19938

<b>STIC-Biotec</b>	h/ChemLib		
From: Sent: To: Cc: Subject:	Tuesday STIC-Bi Leffers,	n, Jeffrey y, September 17, 2002 2:36 PM otech/ChemLib Gerald 846,456	
PLEASE RUSH	<b>I</b> .		
I Approve.			
Jeff Fredman			CRIFE
Original Messa	age		
From: Sent: To: Subject:	Leffers, Gerald Tuesday, September 17, Fredman, Jeffrey RE: 09/846,456	2002 2:27 PM	
SEQ ID NO: 1	(i.e. SEQ ID NO: 1 is I exon_etc ) and 2) th	a denomic dene seglience, SEO ID NO	dly) comprised within the whole ABC1 gene of C: 3 corresponds to the first exon, SEQ ID NO: another examiner without restriction based Thanks, Gerry
Gerald G. Leffers G Examiner, Art U Crystal Mall 1, 703-308-6232	Init 1636		
Original From: Sent: To: Subject:	Message Fredman, Jeffrey Tuesday, September 17, Leffers, Gerald RE: 09/846,456	, 2002 2:24 PM	
Gerald, Given sequence?	this situation, why are	e you not restricting between the seque	nces and requiring election of a single DNA
Jeff			
From: Sent: To: Subjec	ginal Message Leffers, Gerald Tuesday, September 17 Fredman, Jeffrey t: 09/846,456		is application. Total DNA is ≈7 kb. Claims are
directe one of specifi	ed to the whole seque SEQ ID NOS: 1-5. Sication and have not l	ence, or alternatively, a polynucleotide on SEQ ID NOS: 3-5 should be comprised Seen able to find if SEQ ID NO: 2 is fou	is application. Total DNA is ~7 kb. Claims are comprising 20 consecutive nucleotides of any within SEQ ID NO: 1. I have read through the nd within SEQ ID NO: 1. It may be that determine if a single oligo search of SEQ ID Gerry
Searcher: 1	Schreber 308-4292	TYPE OF SEARCH: NA Sequences: 10	VENDOR/COST (where applic.
Phone:	308-4292	AA Sequences:	DIALOG:

Location: CM ( GAO 3

Date Picked Up: 9 (8

Date Completed: 9 (20 Questel/Orbit: \_\_\_\_ Structures: \_\_\_\_\_\_Bibliographic: \_\_\_\_\_ DRLink: Lexis/Nexis: \_\_\_\_\_ Litigation: \_\_\_\_\_\_
Full text: \_\_\_\_\_ Sequence Sys.: Compager WWW/Internet: Searcher Prep/Review: 14 Patent Family: \_\_\_\_\_ Clerical: \_ Other (specify): \_\_\_\_ Online time: 4 Other: \_\_\_\_\_

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Searched:

Sequence Human DNA Homo sapi

Homo sapi Sequence

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
Brewer,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 1 08-NoV-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
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AUTHORS
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Copyright (c) 1993 - 2000 Compugen Ltd.
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PAT 06-FEB-2002

1. Similarity 100.0%; Pred; No. 0; D. 0; Indals coggogacy acquigacy therefore the conservative 0; Mismatches 0; Indals coggogacy acquigacy therefore the conservative 0; Mismatches 0; Indals coggogacy acquigacy therefore the conservative 0; Mismatches 0; Indals cocgacy acquigacy therefore the conservative 0; Mismatches 0; Indals coccagate accacacy acquigacy therefore the conservative of the conservative	0; Gaps 0; tgcaatga 60          TGCAATGA 60	cctcaatt 120            CTCAATT 120	gagagag 180         GaGAGGG 180	aacacct 240	ttcaaca 300             TTCAACA 300	ccatttta 360            CCATTTA 360	ttgggagg 420          TTGGGAGG 420	atggcaaa 480           	cctgtggt 540           CcrGrGGT 540	aagtctaca 600              	ctgtctca 660          	ggaggagg 720          GGAGGAGG 720	gaaaaaaaaa 780               GAAAAAAAA 780	aagtttga 840            AAGTTTGA 840	tccgctct 900           	ittitt 960            TTCTTT 960	
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	Local Similarity 100.0 nes 3231; Conservative 1 acaggcatggtggcaggtgc	gcccagatcgcaccattc 	aaaaaaaaagaatgatttg 	agatggaggtcagggagat 	tttaataacactctctgcttt 	aagttcactttcagaaaacco 	aagatgaagaaacaggccgg 	21 ctgaggccagaggatcg 	81 acctgtct 	cccagctacttgggaggct 	ctgagccatgattggatcact 	aaaaaaagaaatgaaag 	21 gagggggggaggaaggaa 	81 gatgaaacagaggcagaaa 	41 ccccaaaa 	01 cctgggcc          01 ccTGGGCC	61 ttat

٥y	1021	tcgactcactgtaacctctgcctcccgggttcaagcgattctcctgcctcagcctcctga 1080
oy S	80	ataacaggcgcccgccacatctggctaatttttgtattttagtaaagactgggtt 114
ΩĐ	1081	
Qy	14	~
Dp	14	CATCATGTTGGCCAGGTTGGTTTCGAACTCCTGACCTGA
Qy Dp	1201	ctcccaaagtgctgggattacaggcatgagccactgcgcccagctcagatccattt 1260 
οy	1261	taagggcaaacagtccatggtgcaaaggggccatgccaccagagttatgagtacctgg 1
QQ	1261	
ΟŸ	1321	gcctggtggcctccacatgcacttccagggcctgcttgggcctc 138
QQ	1321	ACTCCAGAATTCCTTGCCTGGTGGCCTCCACATGCACTTCCAGGGCCTGCTTGGGCCT
δy	1381	tcctgagtgttgatagaaccactgatgtgagtacctgggcttgagcc 144
qq	1381	TCTATGCGTCTGTCCTGAGGTGTTGATAGAACCACTGATGTGAGTACCTGGGCTTGAGC
δŏ	4	gtgcagctgaatgtctgca 150
Q D	1441	TGGCCTGGAGATCCTGTTGACTGTAGCATGGAGGGGGCTTGTGCAGCTGAATGTCTGCA 150
λ δ	1501	tgcaggtggtggtggagttctggaatatgatggagctggaggtgggaagaagtaggcttg 1560 
ò	56	ggoageteteteatgecaceteattetggecaaaacteaggteaaaetgtgaagagtet 162
Dp	56	9
δy	1621	ccttcaaggtgg
QQ	1621	IGTGAATCTGCCCTTCAAGGTGGCTACAAGGTATCTTTGTCAAGGTAGGAACCTT
Οy	1681	ggcctccacgtgcacttccagggcctgcttgggcctct
qq	1681	TGGCCTCCACGTGCACTTCCAGGGCCTGCTTGGGCCTCTTCTACGGGTCTGTCCTGAGT 1
Oy	1741	cacagtttgacctgagttt 180
qq	1741	TICTATGAATCCTTCAGGGCAGATTCATATTTAGACTCTTCACAGTTTGACCTGAGTTT 1
Qy	1801	
Dβ	1801	GGCCAGAATAAGGTGACATTTAGTTTGTTGGCTTGATGGATG
ΟŸ	1861	gtgtgtaggcctgcattcctactcttgccttttttttgccctccagtgttttgg
QQ	1861	GGTGTGTAGGCCTGCATTCCTACTCTTGCCTTTTTTTTTGCCCCTCCAGTGTTTTGGGT 19
QY	1921	gttttgctccctacagccaaaggcaaacagagaagttggaggtctggagtgg
qq	1921	TIGLICICCCTACAGCCAAAGGCAAACAGAGAAGTTGGAGGTCTGGAGTGGCTAC
Qy	1981	tgcactt
QQ	1981	ITTTACACGACTGCAATTCTCTGGCTGCACTTCACAAATGTATACAAATAC
δλ	2041	gtcctgtgtttttatcacagggaggctgatcaatataatgaaattaaaagggggctggtc 2100
qq	2041	CCGGGGTTTTTTTTTTCACAGGGGGGGCTGATCAATAATGAAATTAAAAGGGGGGCTGGT

Db 3181 AGTGCTCGGTTTCGGGGACTTTGATCCG	RESULT 2 AX092589 LOCUS DEFINITION Sequence 1 from Patent W0011 ACCESSION AX092589 VERSION AX092589.1 GI:13444647 EXTWORDS Number	Σ	ALTHORS Hayden M.R., Brooks-Wilson, a TITLE Compositions and methods for triglyceride levels composition between the composition of the compositio	Ü	/db_xref="taxon:967 BASE COUNT 49549 a 37944 c 41170 g ORIGIN	Query Match 96.8%; Score Best Local Similarity 98.0%; Pred. Matches 3183. Conservative 10: Mi.	caggcatgtgcaggtgcctgtaat	25	122	182	242	302	362	422	482	542	DD 2042U CCAGCTACTTGGGAAGGCTAAGGTGGGAAG
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tgagocatgattggatcactgcactccagcctgggtagacagaca	ggtcgctctcctgggctttgggctttagaaagctcatcttggcctttctgagatcca ggtccgctctcctgggccttgggctttagaaagctcatcttggcctttctgagatcca ggtccgcTTCTGGGCTTTAGAAAGCTCATCTCTGGCTTTCTGAGATCCA cctttcttttttttttttttgacacggagtcttgctctgtcactcaggctggagtgca 	agcctcctgagataacaggcgccaccacatctggctaattttgtatttttagtaa afcctcctgagataacaggcgccaccacatctggctaatttttgtatttttagtaa allililililililililililililililililil		STUTEYATECAGGTGGGAGTTCTGGAATATGATGGAGGTGGAGGTGGGAAGAG A99Cttggggcagctctctcatgccacctcattctggccaaaactcaggtcaaact
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                 cctccagtgttttgggttagttttgctccctacaggccaaaggcaaacagagagttggag
                                                                                                             2204 tegggteetetgagggacetggggageteaggetgggaatetecaaggeagtegee
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http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
sections only once, except for a short overlap.
The true right end of clone RPI1-21787 is at 96717 in this
sequence. The true left end of clone RPI1-21787 is at 96717 in this
sequence. The true left end of clone RPI1-127810 is at 72980 in
this sequence. The true right end of clone RPI1-132810 is at 2000 in
this sequence.
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                derived from a single pUC clone. Restriction digest data confirm the assembly." 92411. .92557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
a 21138 c 20380 g 27526 t
                        Group. Further information can be found at the psymw, sanger ac.uk/HGP/Chr9 RPI1-217B7 is from the library RPCI-11.1 constructed by the group of Pleter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19791 AGATGAAGAAACAGGCCGGGCACAATGGCTAATGCCTGTAATCCCAGCACTTTGGGAGGC 19732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AC026643). Assembly confirmed by restriction digest." 92050. 92163
/note="Sequence from reads from a short insert library
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Institute, Bethesda, MD 20892, USA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Sequence from AF275948 sequenced by National
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/note="Sequence from overlapping clone RP11-122F10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .96717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP11-217B7"
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hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Jan 15, 2002 this sequence version replaced gi:1812468.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30;) an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRI 11-JAN-2002
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Human DNA sequence from clone RP11-217B7 on chromosome 9, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 96717)
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                                                                                                                                                                                                                                                                                                                                                                                                              29000 GTGGAAAAACAGGTAAGAGGCTCTCCAGTGACTTAGTTGGGCGTTATTGTTTTGTTTTGTGG 29059
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      28640 CTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAACGGGGCGGG 28699
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                                                                2804 gaggaggaggagacacaggctttgaccgatagtaacctctgcgctccggtgcagccgaatct
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Qy 26	2626 gcggaccctaagacacctgctgtaccctccaccccaccc	
Oy 2680 Db 17469	2686 aactcctagatgtgtcgtgggcggctgaacgtcgcccgtttaaggggcgggc	
Qy 27 Db 174	746 ccacgtgctttctgctgagtgactgaactacataaacagaggccgggaagggggggg	
Qy 28 Db 173	806 ggagggagagcacaggctttgaccgatagtaacctctgcgctcggtgcagccgaatctat 2865 	
Qy 2866 Db 17289	2866 aaaaggaactagtcccggcaaaaaccccgtaattgcgagcga	
Oy 29 Db 172	2926 cccgcagagccgagccttctctcccgggctgcggcagggcagggcggggagctcc 2985 	
Qy 29 Db 171	2986 gegeaccaacagagccggttctcagggcgctttgctccttgtttttccccggttctgtt 3045 	
Qy 30 Db 171	3046 ttctccccttctccggaaggcttgtcaaggggtaggaaagaagagacgcaaacacaaaagt 3105 	
Oy 31 Db 170	3106 ggaaaacaggtaagaggttttccagtgacttacttgggcgttattgttttgtttcgaggc 3165 	
Qy 31 Db 169	3166 caaggaggettegggaagtgeteggtttegggaeetttgateeggageeceaeteecea 3225 	
Oy 32. Db 169:	26	
RESULT 4 AF287262 LOCUS DEFINITION ACCESSION VERSION VERSION VERSION VERSION VERSION VERSION TETTLE AUTHORS TITLE AUTHORS TITLE JOURNAL	AF287262 201144 bp DNA linear PRI 29-APR-2001 TION Mac Sapiens ATP-binding cassette 1 sub-family A member 1 (ABCA1) and SNAP protein genes, complete cds. AF287262.1 GI:13876612 NS human. NISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rummalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 201144) ORS Qiu,Y. Cavelier,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F. Human and macuse abcral comparative sequencing and transgenesis studies revealing novel regulatory sequences NAL Genomics 73 (1), 66-76 (2001) INE 21251004 Ca (bases 1 to 201144) ORS Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,JF. Direct Submission Submitted (13-JUL-2000) Genome Science Department, Lawrence Berkeley National Laboratory, I Cyclotron Rd, MS 84-171, Berkeley, CA 94720, USA	

Location/Qualifiers 1. .201144 /organism="Homo sapiens"

FEATURES Source

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7010 (33931. 23015) (3819. .58476,72893. .72986,77520. .77661, 79931. .79049,101048. .101169,104452. .104328,117287. .117379, 1222329. .122569,125285. .1255424,125754. .125870, 137876, 130079. .132876,131028. .131749. .131828. .131763, 133708. .133930,135677. .135898,136959. .137163, 138286. .138381,140179. .140350,141340. .14141, 145277. .14219,143123. .140350,141369. .144183, 145471. .145884,150280. .156757, 182778. .155757, 186757. .146859,148527. .148875, 155757, 160942,162417. .162491, 165313,146657. .16042,162417. .162491, 165313,16657. .160942,162417. .162491, 165312,166413. .166959,166588. .166703, 166815. .166959,171017. .171079,171987. .172093, 176142,17216. .175095,176039. .176142,17376. .1775095,177609. .177612,177376. .177619,177850. .181457)
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GYGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKFLLLGKILYTPOTPAT
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EQGICVQWDNLFESPVEEDGFNLFTSVSMMLFNTFLYGVMTWYIEAVFPGQYGIPRPW
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	Oy 3118 agaggeteceagtgacttacttgggcgttattgtttgtttcgaggccaaggaggettc 3177	Z_ W .	AUTHORS Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.  TITLE Regulatory nucleic acid sequences of the abcl gene JOURNAL Patent: WO 0183746-A 3 08-NOV-2001; Aventis Pharma S.A. (FR)  FEATURES  Location/Qualifiers  Location/Qualifiers  Aource  Aorganism="Homo sapiens"  Abs. xref="taxon:9606"  Abs. xref="taxon:9606"  Abs. xref="taxon:9606"	Query Match         89.5%; Score 2893; DB 6; Length 2893;           Best Local Similarity 100.0%; Pred. No. 0;         Do. 0;         Anatches 2893;         Conservative 0; Mismatches 0; Indels 0; Gaps 0;           Qy         1 acaggoatggtggtggtggtatctcagttactcgggaggtggaggttgcaatga 60   [1]

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join(1454. .1674,25831. .25989,40385. .40478,45012. .45153,
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 149034)
Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L., Creng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschild,C., Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N., Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete genomic sequence of the human ABCAl gene: analysis of the human and mouse ATP-binding cassette A promoter.

L Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)

E 20345099

E 2 (bases 1 to 149034)

S Santamarina-F0jo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A., Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E., Francols,T.L. and Brewer,H.B. Jr.

Direct Submission

L Submitted (08-1001200) Molecular Disease Branch, National Institutes of Heath, National Heart, Lung and Blood Institute, Bethesda, MD 20892, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1643)
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Regulation with binding cassette transporter patent: WO 079972-A 3 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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46.0%; Score 1485.4;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 1615; Conservative 0; Mismatches
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413 c 457 g 403
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Sequence 3 from Patent WO0078972.
AX060715
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PAT 22-JAN-2001

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RESULT AX060894 LOCUS

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abc1 polypeptides
Patent: WO 0078971-A 3 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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46.0%; Score 1485.4;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 1615; Conservative 0; Mismatches
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413 c 457 g 403
Sequence 3 from Patent WO0078971.
AX060894
                        AX060894.1 GI:12406271
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ORIGIN
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AC012230 175064 bp DNA linear HTG 22-APR-2000 Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered pieces.
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                      GGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAAATCAAAAGTCCAGGTTTGTGGGGGGAA
                                                                                                                                             aacaaaagcagcccattacccagaggactgtccgccttcccctcaccccagcctaggcct
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                                                              tgaagaagaagcagtaagatgttcctccgggtcctctgagggacctggggagctcagggct
                                                                                                     gggaatctccaaggcagtaggtcgcctatcaaaaatcaaagtccaggtttgtggggggaa
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AC012230.3 GI:7637254
HTG; HTGS_PHASE1; HTGS_DRAFT
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REFERENCE

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97902 98001; gap of 100 bp 98002 103016; contig of 5015 bp in length 103017 103116; gap of 100 bp 103017 103116; gap of 100 bp 103116; gap of 100 bp 10317 109178; contig of 6062 bp in length 109279 117308 117307; contig of 8029 bp in length 117308 117407; gap of 100 bp 124080 124179; gap of 100 bp 124080 131281; contig of 672 bp in length 131282 131381; gap of 100 bp 131382 13181; gap of 100 bp 131862 131819; gap of 100 bp 131862 134819; contig of 6678 bp in length 131282 131819; gap of 100 bp 138159; gap of 100 bp 145592 145591; gap of 100 bp 1500 b
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f 5125 bp in length
8: gap of 100 bp
7200: contig of 1872 bp in length
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3054 bp in length
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contig of 4417 bp in length
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contig of 4402 bp in length
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contig of 4676 bp in length
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93499: contig of 5179 bp in length
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contig of 2943 bp in length
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/clone_lib="RPCI-11 Human Male
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2377 bp i
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f 2568 bp i
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contig of 2831 bp
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contig of 2356 bp
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contig of 2861 bp
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38318: contig of 3919 bp
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/note="assembly_fragment"
2735. .4415
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/db_xref="taxon:9606"
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45549 48116: contig of 1
48117 48216: gap of 1
48217 52618: contig of
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42835: con+
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68437: cont
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71458: con+⁴
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20131: cont
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82113: conf
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34299: con
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                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boquslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boquslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Headrod, A., Horton, L., Howland, J.C., Johnson, R., Mornes, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGrush, R., McCanghlin, J., Marquis, N., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 175064)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 185000; agarosefp
Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; agarose-fp
Quality coverage: 3.2 in Q20 bases; sum-of-contigs
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Center clone name: L2510
Center clone name: L2510
Center clone name: L2510
Center clone name: L2510
Sequencing vector: M33; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 117571 bases at least Q40
Consensus quality: 160940 bases at least Q20
Consensus quality: 160940 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Workact: sequence_submissions@genome.wi.mit.edu
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contig of 1681 bp in length
of 100 bp
contig of 1270 bp in length
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                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-1M10
Unpublished
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COMMENT

Oy 2253 agtaggtcgcctatcaaaaatcaaagtccaggtttgtgggggaaacaaaagcaca 2312	Oy 2433 atcoctcoctcoggctgaggaaactaacaaaggaaaaattgoggaaagcaggattt 2492	2613 gggaegcagaccgcacctaagacacctgctgtaccctccaccccaccccacccc 267 [111111111111111111111111111111111111	Oy 2793 aaggggggggggggggggggggggggggggggggggg	3033 ccccgrtctgtttctccccttctccggaaggcttgtcaaggggaaagagcg 309 301 ccccggrtctgttttctccccrtctccggaaggcttgtcaaggggtaagagagcg 309 302 ccacacacaaagtggaaaacaggtaagaggcttgtcagtgacttactt
	misc_feature 1532917200 misc_feature 170120131 misc_feature 20232587 misc_feature 2268825707 misc_feature 2268825707 misc_feature 2828838138 misc_feature 2828531338 misc_feature 2828531338 misc_feature 2828531338 misc_feature 2828531338	misc_feature //note="assembly_fragment"  misc_feature 3440038318  misc_feature 3441942835  misc_feature 4234042836  misc_feature 4254948116  misc_feature 4554948116  misc_feature 4821752618  misc_feature 5271956592	misc_feature 56693. 59635 misc_feature 56693. 59656 misc_feature 59766. 63661 misc_feature 63762. 68437 misc_feature 63762. 68437 misc_feature 68538. 71458 misc_feature 68538. 71458 misc_feature 71559. 76888 Query Match 38.08; Score 1227.8; DB 2; Length 175064; Best Local Similarity 98.7%; Pred. No. 8.2e-311;	vative  ctggagtggc

353 ACCCAGAGGACTGTCCGCCTTCCCCTCACCCTAGGCCTTTGAAAGGAAACAAAAG 412

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 1167)

Porsch-Ozcurumez,M., Langmann,T., Helmerl,S., Borsukova,H.,
Raminski,W.E., Drobnik,W., Honer,C., Schumacher,C. and Schmitz,G.
The zinc finger protein 202 (znf202) is a transcriptional repressor of atp binding cassette transporter al (abcal) and abcgl gene expression and a modulator of cellular lipid efflux
J. Biol. Chem. 276 (15), 12427-12433 (2001)
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Submitted (05-JAN-2000) Porsch-Oezcueruemez M.K., Institute for
Clinical Chemistry, University of Regensburg,
FRanz-Josef-Strauss-Alleell, 93042 Regensburg, GERMANY
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/gene="ABC-1"
/function="cholesterol efflux regulatory protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="cholesterol efflux regulatory protein"
315 c 327 g 247 t
                                              ABC-1 gene; ATP-binding cassette transporter-1; promoter
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transporter-1, 5'UTR and promoter region
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="leukocyte"
1. .1167
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Porsch-Oezcueruemez,M.K.
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AJ252201.1 GI:12053757
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/gene="ABC-1"
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AF128623S1 1167 bp DNA linear PRI 23-JUN-2000 monographic assette transporter 1 (ABCAL) gene,
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Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Audizerat, B.E., Fielding, C.J. and Kane, J.P.
Analysis of habCl gene 5' end: additional peptide sequence, promoter region, and four polymorphisms
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828 CGGGGGGGGGGGGGGGGGGGGGGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCA 887
                                                                                                              aggaagcaaattccactggtgcccttggctgccgggaacgtggactagagagtctgcggc
                                                                                    3095 aacacaaaagtggaaaacaggtaagaggctctccagtgac 3134
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AF258623.2 GI:8677405
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                                                                          Submitted (20-APR-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
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                                                                                                                  Truncisco, A. Tronger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizeatt, B.E., Fielding, C.J. and Kane, J.P.
Direct Submission
Submitted (23-JUN-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, Francisco, CA 94143-0130, USA
Sequence update by submitter
On Jun 23, 2000 this sequence version replaced gi:7769713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atgttcctctcgggtcctctgagggacctggggagctcaggctgggaatctccaaggcag 2254
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Biochem. Biophys. Res. Commun. 271 (2000) In press 24 to 1167)
Pullinger, C.R., Hakamatch, H., Duchateau, P.N., Eng.C., Aquizerat, B.E., Fielding, C.J. and Kane, J.P.
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/chromosome="9"
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/gene="ABCAl"
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Homo sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING.
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Birren, B., Linton, L., Nusbaum, C. and Land
Homo sapiens chromosome, clone RP11-1N10
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Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                     Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6705871. All repeats were Identified sing RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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Zimmer, A. and Zody, M.
Direct Submission
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41705 CCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAAAAAGAGACGC 41764
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AC012230.3 GI:7637254
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AC012230/c
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                                                                                             1582313 gap of 100 bp 10 length 159182 contig of 852 bp in length 159182 gap of 100 bp 100 bp
                    p of 100 bp contig of 866 bp in length
56197: contig of 868 bp in length
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57163: cont
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95.9%;
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Best Local Similarity 95.99
Matches 750; Conservative
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AC012230 175064 bp DNA linear HTG 22-APR-2000 Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered pieces.
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1 (bases 1 to 175064)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-1M10
                                                          Center clone name: 1_M_10

Center clone name: 1_M_10

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 117571 bases at least Q40
Consensus quality: 145749 bases at least Q20
Consensus quality: 165749 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; sum-of-contigs
Quality coverage: 3.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: L2510
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100 bp 6672 bp in length 100 bp f 7102 bp in length

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117408 11247793 config of 6672 bp in length 112408 124179; gap of 100 bp 124180 131281 contig of 7102 bp in length 131282 1313181; gap of 100 bp 131882 1318159; gap of 100 bp 131860 138159; gap of 100 bp 145492 145591; gap of 100 bp 145592 157391; contig of 7332 bp in length 15732 157391; contig of 100 bp 157392 157391; contig of 100 bp 157392 157391; contig of 17573 bp in length 157392 157491; gap of 100 bp
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/note="assembly_fragment"
52719. .56592
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1104. .2634
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5886. .7879
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17301. .20131
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22688. .25707
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/note="assembly_fragment"
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/note="assembly_fragment"
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7980. .9686
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/db_xref="taxon:9606"
/clone="RP11-1M10"
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71559. .76888
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NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                2635 2734: gap of 100 bp 2735 4415: contig of 1681 bp in length 4416 4515 5785: contig of 1270 bp in length 5786 5885: gap of 100 bp in length 7880 7979: contig of 1994 bp in length 7880 7979: gap of 100 bp 7980 9686: contig of 1707 bp in length 7980 9686: contig of 1707 bp in length
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103117 109178; contig of 6062 bp in length
109179 109278; gap of 100 bp
109279 117307; contig of 8029 bp in length
                                                                                                                                                                  of 100 bp
contig of 1531 bp in length
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31338: contig of 3054 bp in length
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88419 42835: contig of 4417 bp in length
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45448; contig of 2513 bp in length
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2568 bp in length
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63661: contig of 3926 bp in length
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68437: contig of 4676 bp in length
68537: gap of 100 bp
71458: contig of 2921 bp in length
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5330 bp in length
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88220: contig of 6007 bp in length
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22587: contig of 2356 bp in length
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contig of 2943 bp in length
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contig of 4302 bp in length
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103016: contig of 5015 bp in length
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82113: cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                       1678 CCGGCATGGTGGCAGGTGCCTGTAATCTCAGCTACTCGGGAGGTGGAGGTTGCAATGAG 1619
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                                              cagggcatggtggcaggtgcctgtaatctcagttactcgggaggtggaggttgcaatgag 61
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Homo sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING.
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 Pred. No. 5.7e-134;
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Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Flerre, N., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanhan, A., Talamas, J., Teefaye, S., Theodore, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                             Submitted (16-7AM-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6705871.
All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasKer.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissionsegenome.wi.mit.edu
------ Project Information
Center project name: L2512
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1835 1934: gap of 100 bp
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contig of 851 bp in length
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10 19109: 39 of 100 bp 11 1996; contig of 857 bp in length 100 bg 2021; contig of 855 bp in length 100 bg 2021; contig of 855 bp in length 100 bg 2021; gap of 100 bp 100 
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44853 4524: contig of 872 bp in length
45725 45643: contig of 819 bp in length
4664 46743: gap of 100 bp
4674 46743: gap of 100 bp
4674 47699: contig of 856 bp in length
4700 47699: gap of 100 bp
4770 48551: contig of 852 bp in length
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1068 41913; contig of 846 bp in length
1914 42013; gap of 100 bp
2014 42824; contig of 811 bp in length
2825 42924; gap of 100 bp
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12925 43776: contig of 852 bp in length
13777 43876; gap of 100 bp
13877 44752: contig of 876 bp in length
                                                        17073 17172: gap of 100 bp
17173 18041: contig of 869 bp in length
18042 18141: gap of 100 bp
18142 19009: contig of 868 bp in length
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18652 49485: contig of 834 bp in length
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17072: contig of 849 bp in length
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Pred. No. 2.3e-118;
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66684: contig of 844 bp in length
66784: gap of 100 bp
6751: contig of 867 bp in length
67751: gap of 100 bp
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04: gap of 100 bp 52372: contig of 868 bp 72: gap of 100 bp 53328: contig of 856 bp
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                                                                                                                                                                                                                      HTG 13-JUL-2000
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1 (bases 1 to 90698)]
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo. sapiens, clone RP11-24J9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6705761.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: Project Information
Center project name: 14483
Center clone name: 24_J_9
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                                                                                      67102 TGATCCGGAGCCCCACATCCCC 67081
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COMMENT

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14685 14784; gap of 100 bp 14785 15622; contig of 878 bp in length 15763 15762. gap of 100 bp 15763 16677; contig of 915 bp in length 1678 16777; gap of 100 bp 16778 1779; gap of 100 bp in length 1779 1778; gap of 100 bp in length 1860 18779; gap of 100 bp in length 1863 19732; gap of 100 bp in length 19633 19732; gap of 100 bp in length 19732; gap of 100 bp in length 19733 20634; contig of 902 bp in length
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10858 11732: contig of 875 bp in length
11733 11832: gap of 100 bp
11833 12739: contig of 907 bp in length
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f 883 bp in length
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34435: contig of 888 bp in length
34535: gap of 100 bp
35433: contig of 898 bp in length
35533: gap of 100 bp
36440: contig of 907 bp in length
    in length
                                                                                     914 bp in length
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21620: contig of 886 bp in length
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31453: contig of 906 bp
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37523 38402: contig of 880 bp
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1 53250: contig of 870 bp in length 50250: contig of 870 bp in length 100 bp 10
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                                                                                                                                                                                                                                                                                                                                                                                             43357; contig of 858 bp in length 445; gap of 100 bp 4525; contig of 899 bp in length 455; gap of 100 bp 645325; contig of 869 bp in length 645; gap of 100 bp 100 
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                                                39480: gap of 100 bp
440407: contig of 927 bp in length
4507: gap of 100 bp
41405: contig of 898 bp in length
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39380: contig of 878 bp in length
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45325: con
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Query Match 14.8%; Score 478.8; DB 2; Length 90698; Best Local Similarity 90.8%; Pred. No. 2.3e-114; Matches 543; Conservative 0; Mismatches 49; Indels 6; Gaps

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                             1736436 seqs, 858457221 residues
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Listing first 45 summaries
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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human ABC1 genomic Nucleotide sequenc Nucleotide sequenc Human CDNA sequenc Human reproductive Human nervous syst Human nervous syst Human innnine/haema
SUMMARIES	AAF92831 AAF24681 AAF24703 AAH04729 AAH17451 AAL05355 ABA16699 ABA16699
ЭВ	22222222
% Query e Match Length DB	96.8 183999 46.0 1643 10.4 1750 10.2 20645 10.2 5075 10.1 5075
% Query Match	96.8 4.60 10.4 4.00 10.2 10.2 10.0
Score	3127.8 11485.4 1485.4 1485.4 336 330.8 330.6 325.8
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LXR (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates or RXR-mediated transcriptional activity -

Claim 8; Fig 1; 317pp; English.

ø The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.

Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;

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The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apollpoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1
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10; are useful for developing pharmaceutical agents for the treamfact of meart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia. 1879 1464 1524 1584 1644 1938 2058 1704 gcctgcttgggcctcttctacgggtctgtcctgagtcttctatgaat---ccttcagggc 1761 1821 2117 311 430 191 251 371 490 550 610 670 26; Gaps ggctccacatgcacttccagggcctgcttgg--ctcttctatgggtctgtcctgagtgtt 73 gatagaaccactgatgtgagtacctgggcttgagccgtggcctggagatcctgttgactg tagcatggagggggttgtgcagctgaatgtctgcatgcaggtggtgggagttctggaat tagcatggaggggcttgt-cagctgaatgtctgtatgcaggtggtgggagttctggaat atgatggagctggaggtgggaagaagtaggcttgggggcagctctctcatgccacctca ttctggccaaaactcaggtcaaactgtgaagagtctaaatgtgaatctgccttcaaggt agattcatatttagactcttcacagtttgacctgagttttggccagaataaggtgacatt tagtttgttggcttgatggatgacttaaatatttagac-atggtgtgtaggcctgcatt cctactcttgcctttttttttgccctccagtgttttgggtagttttgct-ccctacag agggaggctgatcaataatgaaattaaaagggggctggt-ccatattgttctgtgttt atgatggagctggaggtgggaagaagtaggcttgggggcagctctctcatgccacctca ggctacaaaggtatcttgtcaaggtaggagaccttgtggcctccacgtgcacttccagg tagtttgttggcttgatgaatgacttaaatatttagacatatggtgtgtaggcctgcatt cctactcttgccttttttgcccctccagtgttttgggtagttttgctcccctacag ccaaaggcaaacagagaagttggaggtctggagtggctacataattttacacgactgcaa ccaaaggcaaacagataagttggaggtctggagtggctacataattttacacgactgcaa ttctctggctgcacttcacaaatgtatacaaactaaatacaagtcctgtgtttttatcac Score 1485.4; DB 22; Length 1643; Pred. No. 5e-305; 0; Mismatches 6; Indels 26; Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other; 46.0%; 98.1%; Query Match
Best Local Similarity 98.1:
Matches 1615; Conservative ttg-1345 1525 312 372 431 671 16 1405 74 133 192 1585 252 1645 1705 1762 491 1880 1939 1999 2118 1822 551 2059 791 1465 8888888888 g g q 요 g à ò g ò ò ò à δ g οy a Qγ g à qq à g à a ò g à a ò

AAF24703 standard; DNA; 1643 BP. (first entry) sapiens 20-APR-2001 AAF24703; 842 2358 1142 2238 2298 2478 2538 1262 1557 1022 2418 1082 2718 2778 2898 1202 2598 2658 1322 1377 2838 1497 1617 Homo 1437 RESULT AAF24703 à g δ g ŏ qq ò g ŏ dd Ω qq δ Op ð g δ q ò q δ d ò qq δ q tgaagaagaagcagtaagatgttcctctcgggtcctctgagggacctggggagctcaggct 2237 gene is localised to chromosome 9q22-9q31. The ABC1 genes and 2178

2777 962 aacaaaagcagcccattacccagaggactgtccgccttcccctcaccccagcctaggcct 1021 ttgaaaggaaacaaaagacaagacaaaatgattggcgtcctgagggagattcagcctaga 1081 getetetetececccaatecetecetecgetgaggaaactaacaaaggaaaaaaattg 1141 actagagagtctgcggcgcagccccgagcccagcgcttcccgcgcgtcttaggccggcgg 1261 Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss. 902 gggaatctccaaggcagtaggtcgcctatcaaaaatcaaagtccaggtttgtggggggaa gggaatctccaaggcagtaggtcgcctatcaaaaatcaaagtccaggtttgtggggggaa aacaaaagcagcccattacccagaggactgtccgccttcccctcaccccagcctaggcct ttgaaaggaaacaaaagacaagacaaaatgattggcgtcctgagggagattcagcctaga getetetetececeaateeteeteeteeggetgaagaaactaacaaaggaaaaaaattg cggaaagcaggatttagaggaagcaaattccactggtgcccttggctgccgggaacgtgg actagagagtctgcggcgcagcccgagcccagcgttcccgcgcgctttaggccggcgg ----cccaccccacccacctcccccaactccctagatgtgtcgtgggcggctgaacg tegecegittaagggggggggecegggetecacgitgettetgetgagtgaetgaactaca taaacagaggccgggaaggggggggggggaggaaggaacaggctttgaccgatagtaa cctctgcgctcggtgcagccgaatctataaaaggaactagtcccggcaaaaaccccgtaa ttgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctcccgg ccccaccccaccccaccctccccccaactccctagatgtgtcgtgggcggctgaacg cctctgcgctcggtgcagccgaatctataaaaggaactagtcccggcaaaaaccccgtaa region of the human ABC1 Nucleotide sequence of the 5' flanking 2958 gctgcggcagggcagggcggggagctc 2984 getgeggeagggeagggeagete 1643

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The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) I gene. ABCI resides in cell membranes and utilises ATP Mydrolysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABCI is defective in Tangher disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 9422-9431. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
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99US-0166573.
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WO200078971-A2
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19-NOV-1999;
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Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonuclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a least 15 nucleotides; or (b) a combination of sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a coligonucleotide comprises as 1 east 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the approximation of the full-length cDNAs. The primers are also useful for the the full-length cDNAs. The primers also useful for the checking and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers also useful for AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
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   cctctgcgctcggtgcagccgaatctataaaaggaactagtcccggcaaaaaccccgtaa
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Wakamatsu A, Nagai K,
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                                                                                                                                                                                                                                                                                gctgcggcagggcagggcgggagctc 2984
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Sugiyama T, Wakamatsu
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2000JP-0118776.
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09-JUN-2000; 2000JP-0241899
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11-JAN-2000;
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Ishii S,
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AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                          gggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggcgc 3015
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                                                                                     10.4%; Score 336; DB 22; Length 763; 100.0%; Pred. No. 9.1e-62; tive 0; Mismatches 0; Indels
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, Otsuki T
                                                  Sequence 763 BP; 137 A; 205 C; 260 G; 158 T; 3 other;
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A, Nagai K,
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T, Wakamatsu
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27-ANG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
09-JUN-2000; 2000JP-0241899.
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                          of the present invention.
                                                                                                                 Conservative
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                                                                                                    Best Local Similarity
Matches 336; Conserv
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The present invention describes primer sets for synthesising 5602 (ill-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligounclectide complementary to the complementary strand of a polyvuclectide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polyvucleotide which comprises a 5'-end sequence and an oligonuclectide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence of an oligonucleotide comprises a 1'-end sequence of polynucleotide which comprises a 1'-end sequence of polynucleotide which comprises a 1'-end sequence of the primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the price contains encoded by the full-length cDNAs. The primers are also useful for the AH13632 to AAH13632 and AAH13633 to AAH3633 represent human cDNA sequences; and AAH13632 to AAH13632 or FPARESENT human annon acid sequences; and AAH13632 to AAH13632 or FPARESENT human annon acid sequences; and AAH13632 to AAH13632 or FPARESENT human annon acid sequences; and the exemplification and an annon acid sequences; and an the exemplification and an annon acid sequences; and an annon acid sequences.
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2000US-0218290.
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Human; reproductive system related antigen; reproductive system disorder;
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(first entry)

21-NOV-2001 AAL05355;

cancer; gene therapy; ds

Homo sapiens

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2000US-0249215.
2000US-0249216.
2000US-0249217.
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20000S-0249264.
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Ruben SM;
                            (HUMA-) HUMAN GENOME SCI INC
2001US-0259678
                                                         Barash SC,
                                                           Rosen CA,
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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                                          Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                                                                                           Disclosure; SEQ ID NO 8043; 1297pp + Sequence Listing; English
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Best Local Similarity 61.2
Matches 590; Conservative
          WPI; 2001-465570/50
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
1081 gataacaggcgcccgccaccacatctggctaatttttgtattttagtaaagactgggtt 1140
                                      1141 tcatcatgttggccaggttggtttcgaactcctgacctgaggtgagctgccaccttggc 1200
                                                                                                                                                                                  Human nervous system related polynucleotide SEQ ID NO 9030.
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04-FEB-2000; 2000US-0180628.

02-MAR-2000; 2000US-0180634.

15-MAR-2000; 2000US-0180874.

17-MAR-2000; 2000US-0180874.

18-APR-2000; 2000US-0190874.

19-MAY-2000; 2000US-020515.

19-MAY-2000; 2000US-020515.

28-JUN-2000; 2000US-020515.

30-JUN-2000; 2000US-0215135.

30-JUN-2000; 2000US-0217487.

11-JUL-2000; 2000US-0217513.

14-AUG-2000; 2000US-0225213.
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13-OCT-2000;
20-OCT-2000;
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovariant cancer and other cancers of the adrenal gland, bone, marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hyproiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and cepilepsy; and (f) infectious diseases such as viral, bacterial, fungal Note: The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification, but was obtained in electronic format directly
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2000US-0254097.
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cancers and metastases -
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06-DEC-2000;
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10.2%; Score 330.6; DB 22; Length 5076; 65.0%; Pred. No. 2.1e-60;
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                               299; Indels
                               0; Mismatches
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587; Conservative
    Query Match
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds. 2000US-0179065. 2000US-0180628. 2000US-018664. 2000US-0189374. 2000US-0199174. 2000US-0198123. 2000US-0205515. 2000US-0205515. 2000US-021515. 2000US-0215135. 2000US-0216880 2000US-021487 2000US-0214867 2000US-0228290 2000US-0220964 2000US-0224518 2000US-0224518 2000US-0226279. 2000US-0226681. 2000US-0226868. 2000US-0227009. 2000US-0228924. 2000US-0229287. 2000US-0229343. 2000US-0229344. 2000US-0229345. 2000US-0229509. 2000US-0225268 2000US-0225270 2000US-0225758 2000US-0225759 2000US-0225267 2000US-0225447 2000US-0227182 17-JAN-2001; 2001WO-US01334 WO200159063-A2. 18 - AUG - 2000)
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35 - AUG - 2000)
36 - A 07-JUL-2000; 11-JUL-2000; 11-JUL-2000; 14 - AUG - 2000; Homo sapiens 14-JUL-2000; 26-JUL-2000; 14-AUG-2000; -AUG-2000; 14-AUG-2000; 14-AUG-2000; 16-AUG-2001 

2000US - 0233063 2000US - 0234233064 2000US - 0234223 2000US - 02344997 2000US - 02344997 2000US - 02344997 2000US - 0235484 2000US - 0235834 2000US - 0235834 2000US - 0235836 2000US - 0235836 2000US - 023680 2000US-0240960. 2000US-0241785. 2000US-0241786. 2000US-0241786. 2000US-0241808. 2000US-0241809. 2000US-0241826. 2000US-0242221. 2000US-0244617. 2000US-0246610. 2000US-0246611. 2000US-0246613. 2000US-0249207. 2000US-0249208. 2000US-0249215. 2000US-0249216. 2000US-0249217. 2000US-0251988. 2000US-0256719. 2000US-0251479. 2000US-0246474. 2000US-0246475. 2000US-0246475. 2000US-0246526 2000US-0246477 2000US-0246478 2000US-0246523 2000US-0246524 2000US-0246527 2000US-0246532 2000US-0246609 2000US-0249209 2000US-0249210 0000US-0249211 20000S-0249212 20000S-0249213 2000US-0249214 2000US-0249218 2000US-0249244 2000US-0249245 2000US-0249265 2000US-0249297 2000US-0249299 2000US-0249300 2000US-0251160 2000US-0251030 2000US-0249264 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 21-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 27-SEP-2000; 27-SEP-2000; 27-SEP-2000; 27-SEP-2000; 27-SEP-2000; 27-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 02-061-2000; 02-061-2000; 02-061-2000; 02-061-2000; 03-06 20-OCT-2000; 20-OCT-2000; 01-NOV-2000; 08-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 2000US-0232397. 2000US-0232398. 2000US-0232399. 2000US-0232400.

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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the genes are The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune throughly cancer and other cancer of sisease, allergies, conditing disease, multiple sclerosis, rheumatch arthritis and ulcerative collitis; (c) cardiovascular disorders such as myocardial ischaemias;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
and parasitic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2922 AGAGAGAAAAAAAGAGTCTTGATAAGGAACTTGGCATAACTAAATAATTTGGAAGATAAA 2863
                                                                                                                                                                                                                                                                                          Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3221 GGCCTGGTGCATTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGAGCGGA 3162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3161 TCACCTGAGGTCAGGAGTTTGAGACAAGCCTAGCCAACATGGTGAAACCC-CCATCTCTA 3103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3042 AGGCTGAGGCAGAAGAATTGCTTGAACCCAGGAGGTGGAGGTCGCAGTGAGCCGAGATCA 2983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 ggccgggcacaatggctaatgcctgtaatcccagcactttgggaggctgaggccagagga 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                555 aggetaaggtgggaggatcgettgageecagggagteaagtetaeactgageeatgattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          615 gatcactgcactccagcctg---ggtagacagagcaagaccctgtctcaaaaaaagaaa
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                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 9032; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5075 BP; 1437 A; 1054 C; 1187 G; 1397 T; 0 other;
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1larity 64.7%; Pred. No. 2.2e-59;
Conservative 0; Mismatches 302;
             08-DEC-2000; 2000US-0251868.

08-DEC-2000; 2000US-0251869

08-DEC-2000; 2000US-0251989.

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Matches 584; Conserv
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2862 AAGTCAAGGAAGCTTCAGGATCTTTTACCAATTATTTTTAAAGTCTAAAGTGACAACCTA 2803

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tcatgttggccaggttggtttcgaactcctgacctgaggtgagctgccaccttggcctc 1203
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                                                                                                                                                                                       aacaggcgcccgccacacatctggctaatttttgtatttttagtaaagactgggtttca 1143
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                                                               2745 GCTGGGTAGAATCAGGGGCACTTGCTTTCCCGTGGAGGGTCTTCAGGTGACGTTCTTATC 2686
                                                                                                          2685 AACTICIGACCAACCIGGCCAAIGCITCCIIGGAAIAAITIITITITITITITITITITITI 2626
                                                                                                                                                                                                                                                                                                                                  CCAAAGTIGCAGGGATTACAGGCATGAGCCACCGTGCCCAGACAATTITITITITITT 2327
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                                                                                                                                                                                                                                                                                792 ggcagaaagactttacgtaaattgctcatcatgtggttgtcaagtttgaccccaaaaccc
                                           852 aatttattgaccaaggttattctttgactgaggcaagggggtccgctctcctgggccttg
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                                                                                      AAK82208 standard; DNA; 36785 BP.
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20000S-0208467.
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08-DEC-2000;
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Rosen CA, Barash SC, Ruben SM

(HUMA-) HUMAN GENOME SCI INC

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 37020; 3071pp + Sequence Listing; English.

AMK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the

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represent sequences used in the exemplification of the present invention.
                         diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
protein. (I) proteins and polynucleotides may be used to prevent,
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Pred. No. 9.8e-59;
0; Mismatches 307;
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63.5%;
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antialiaergic; antiulcer; anticonvulsant; antimagal; antiparasitic; cardiatbetic; antiune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                 Human nervous system related polynucleotide SEQ ID NO 11476.
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The first conditions e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune chaemly autoimmune thyroiditis, diabetes mellitus, Crohn's colitis; (c) cardiovascular disorders such as mycoardial ischaemias; (d) wound healing; (e) neurological diseases e.g. crebral anoxia and parasitic infections.

Note: The sequence data for this patent did not form part of the Note: The sequence data for this patent did not form part of the from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
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2000US-0251479.
2000US-0251856.
2000US-0251868.
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2000US-0251988.
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05-JAN-2001; 2001US-0259678.
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
20570 GCCTGGCTAATTTTTGTATTTTAGTAGACAGGGTTTTACCATGTTGGCCAGGCTGAT 20511
                                                                                                                         20985 GTAGAAGTGATCAGATATTTATCTGCATAAATAATAAAGGTAGAAAGTAATTCATATT 20926
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                                                   768 aagaaaaaaaaaagatg----aaacagaggcagaaagactttacgtaaattgctcat
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S (HUMA-) HUMAN GENOME SCI INC. Barash SC, WPI; 2001-451937/48 Rosen CA,

Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune charcimune thyroiditis, diabetes mellitus, Crohn's disease, anemal, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple scalerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. crebral anoxia and epilepsy; parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. healing; (e) neurological diseases e.g. cerebral anoxia and epile and (f) infectious diseases such as viral, bacterial, fungal and musculoskeletal cancers and also for testing and detection e.g. Example 2; SEQ ID NO 2536; 781pp + Sequence Listing; English. diagnosis 

Sequence 23934 BP; 7023 A; 4365 C; 4761 G; 7785 T; 0 other;

9 2594 tttctcacataaagaccttacttaggaggccagacgtggtggctcatgcctataatccca 2653 2654 gcactttgggaggccgaggctggcagatcgcttgagtgcaggagtttgagaccagcatgg 2713 2714 gcaacatggcgaaaccccatctctacaaaaata---caaaattaaccaggtgttgtggc 2770 1831 ggcggaggttgcagtgagccgagatcatgccactgcactctagcctggg-cgacagagca 2889 3130 attcagagatgaagccagaaggaactctgggttgaggagaaggcattggggagccagcgg 3189 2950 gtagaagtgatcagatatttatctgcataaataataaaggtagaaagtaattcatattt 3009 3070 cataaaattttctactttgggagacagaaaaatcatggaaatgttccttgaaaaatttt 3129 707 767 587 647 348 tototocattttaaagatgaagaaacaggocgggcacaatggotaatgcotgtaatcoca 407 467 768 aagaaaaaaaaaaagatg----aaacagaggcagaaagactttacgtaaattgctcat 820 Indels 34; Gaps gcactttgggaggctgaggccagaggatcgcttgagctccagagtttgagaccagcctgg 468 ataacatggcaaaaccctgtctctacaaaaaaatacaaaaattagatgggtgtggtgg 528 atgcacctgtggtcccagctacttgggaggctaaggtgggaggatcgcttgagcccaggg 588 agtcaagtctacactgagccatgattggatcactgcactccagcctgggtagacagagca catgtggttgtcaagtttgaccccaaaacccaat------ttattgaccaaggtta ttetttgaetgaggeaagggggteegeteetgggeettgggetttagaaageteatet 3010 taagaaggaacaattggggtttcataactcatgaagagttaaatgagttcaaaagaggga DB 22; Length 23934; 9.9%; Score 320.4; DB 22; 64.2%; Pred. No. 4.6e-58; live 0; Mismatches 296; Query Match 9.9 Best Local Similarity 64.2 Matches 592; Conservative 408 á d δ g ò g ŏ pp ğ g ò g g g ò ōγ δ d

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PR 14-AUG-2000; 2000US-0225770.
PR 14-AUG-2000; 2000US-0225751.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225758.
PR 12-AUG-2000; 2000US-0225759.
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PR 22-AUG-2000; 2000US-0225787.
PR 22-AUG-2000; 2000US-0225871.
PR 22-AUG-2000; 2000US-022948.
PR 22-AUG-2000; 2000US-022948.
PR 23-AUG-2000; 2000US-022948.
PR 23-AUG-2000; 2000US-022948.
PR 01-SED-2000; 2000US-022948.
PR 01-SED-2000; 2000US-023948.
PR 01-SED-2000; 2000US-0231413.
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PR 14-SED-2000; 2000US-0231499.
PR 14-SED-2000; 2000US-0231499.
PR 14-SED-2000; 2000US-0231499.
PR 25-SED-2000; 2000US-02317039.
PR 25-SED-2000; 2000US-02317039
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2000US-0251988.
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(HUMA-) HUMAN GENOME SCI INC

Ruben SM Rosen CA, Barash SC,

WPI; 2001-451937/48.

Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis

Example 2; SEQ ID NO 2544; 781pp + Sequence Listing; English.

for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antibagonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune hypoiditis, diabetes mellitus, Crohn's disease, multiple scierosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. parasitic infections.

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21104 GCGGGGGGTTGCAGTGAGCCGAGATCATGCCACTGCACTCTAGCCTGGG-CGACAGAGCA 21046
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Pred. No. 4.6e-58;
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                                                                   Human reproductive system related antigen DNA SEQ ID NO: 7210.
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2000US-0232397
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                                                  (first entry)
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18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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14-SEP-2000;
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16-MAR-2000;
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2000US-0232399.
2000US-0232400.
2000US-0233403.
2000US-0233064.
2000US-0233064.
2000US-0234274.
2000US-02344997.
2000US-023484.
2000US-023484.
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20000S-0236368.
20000S-0236369.
20000S-0236370.
20000S-0236370.
20000S-0237039.
20000S-0237039.
20000S-0237039.
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2000US-0241785
2000US-0241786
2000US-0241808
2000US-0241809
2000US-0244617
2000US-0244617
2000US-0246417
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2000US-0240960.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2594 titotoacataaagacottacttaggaggocagacgtggtggctcatgcctataatocca 2653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2714 gcaacatggcgaaaccccatctctacaaaaata---caaaattaaccaggtgttgtggc 2770
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                                                                                                                                                                                                                                                               Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 7210; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23934 BP; 7023 A; 4365 C; 4761 G; 7785 T; 0 other;
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Pred. No. 4.6e-58;
0; Mismatches 296; Indels
                                                                                                                                                                                                       Ruben SM;
                2000us-0256719.
2000us-0251479.
2000us-0251856.
2000us-0251868.
2000us-0251869.
2000us-0251989.
                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
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Local Similarity 64.2%;
                                                                                                                                        05-JAN-2001; 2001US-0259678
   2000US-0251988
                                                                                                                           2000US-0254097
                                                                                                                                                                                                                                                                                                                                                                                                         protein of the invention.
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05-DEC-2000; 2
05-DEC-2000; 2
06-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
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tcaagcgattctcctgcctcagcctc-----ctgagataacaggcgcccgccacac 1102
                                                                                                                                        tcactcaggetggagtgcagtggcatgatetegaetcactgtaacetetgeetecegggt 1050
                                                                     3130 attcagagatgaagccagaaggaactctgggttgaggagaaggcattggggagccagcgg 3189
                                                                                                                                                                                                                                                                                                                                                                        Human; respiratory antigen; respiratory disorder; throat disorder; lung disorder; nose disorder; lung cancer; gene therapy; cytostatic; anti allergic; anti asthmatic; anti inflammatory; olfactory; respiratory active; ds.
                                                                                                                                                                                                                                                                                                                                                       Genomic sequence #183 encoding for novel human respiratory antigen
                   3190 tagggactggagagatctg----gaagcataagaaggaatgagacagagtatcactctg
                                                                                                                                                                                                                                                                                               BP
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ID AAS28343 standard; DNA; 23934
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2000US-0205515.
2000US-020467.
2000US-0214886.
2000US-0215135.
2000US-021647.
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2000US-0189874.
2000US-0190076.
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2000US-0224519.
2000US-0225213.
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2000US-0180628.
2000US-0184664.
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2000US-0217496.
2000US-0218290.
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2000US-0225266
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28-JUN-2000;
30-JUN-2000;
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17-MAR-2000;
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AUG-200	SEP-2000	0071-200 007
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AAS28161-AAS28764 represent genomic sequences encoding for novel human respiratory antigens.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel human respiratory antigens (AAU17685-AAU17975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis), lung disorders e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the respiratory tissues e.g. lung cancer. The polynucleotide sequences of the invention are useful in gene therapy and antisense therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide for treating, preventing and, or prognosing disorders related to the respiratory system including respiratory cancers and also for testing and detection e.g. diagnosis \dot{}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA, Barash SC, Ruben SM;
                                 200005-0246532
200008-0246609
200008-02466113
200008-0249207
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200008-0251868
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                       2000US-0246528
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11-DEC-2000;
05-JAN-2001;
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Sequence 23934 BP; 7785 A; 4761 C; 4365 G; 7023 T; 0 other;

06-NOV-2001 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20865 CATAAAATTTTCTACTTTGGGAGACAGAAAAATCATGGAAATGTTCCTTGAAAAATTTT 20806
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                                                                                                                        21281 GCACTTTGGGAGGCCGAGGCTGGCAGATCGCTTGAGTGCAGGAGTTTGAGACCAGCATGG 21222
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                                                                                                gcactttgggaggctgaggccagaggatcgcttgagctccagagtttgagaccagcctgg 467
                 Gaps
                                                                                                                                                    468 ataacatggcaaaaccctgtctctacaaaaaaaaatacaaaaattagatgtgtggtg
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                34;
64.2%; Pred. No. 4.6e-58;
Live 0; Mismatches 296; Indels
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              592; Conservative
 Best Local Similarity
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                          Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26254.
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccibe production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
capteression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
cupplement disorders may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
concern and cancer metastases of haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK64703
concerns and cancer metastases of haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK64703
concerns and cancer metastases of haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK64703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 26254; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                          Ruben SM;
                       2000US-0251869.
2000US-0251989.
2000US-0251990.
2000US-0254097.
                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
2000US-0251868
                                                                                                                      05-JAN-2001; 2001US-0259678
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9 2654 gcactttgggaggccgaggctggcagatcgcttgagtgcaggagtttgagaccagcatgg 2713 2714 gcaacatggcgaaaccccatctctacaaaaata---caaaattaaccaggtgttgtggc 2770 2771 acatacctgtagtcccagctactgaggaggctgaggcacaagaattgcttgagcctggga 2830 2890 agactetgtateaaaaaaaaaaaaaaaaaaaaaaaaaeeettaggaaetetaagteaa 2949 2950 gtagaagtgatcagatatttatctgcataaataaaaaggtagaaagtaattcatattt 3009 2594 tttctcacataaagaccttacttaggaggccagacgtggtggctcatgcctataatccca 2653 588 agtcaagtctacactgagccatgattggatcactgcactccagcctgggtagacagagca 647 467 528 atgcacctgtggtcccagctacttgggaggctaaggtgggaggatcgcttgagcccaggg 587 768 aagaaaaaaaaaagatg-----aaacagaggcagaaagactttacgtaaattgctcat 820 348 tetetecattttaaagatgaagaaacaggeegggeacaatggetaatgeetgtaateeca 407 Score 320.4; DB 22; Length 23934; Pred. No. 4.6e-58; 0; Mismatches 296; Indels 34; Gaps gcactttgggaggctgaggccagaggatcgcttgagctccagagtttgagaccagcctgg 9.9%; Best Local Similarity 64.2 Matches 592; Conservative Query Match 408

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Search completed: September 20, 2002, 03:08:22 Job time: 10571 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 23:25:11; Search time 110.16 Seconds (without alignments) 7204.447 Million cell updates/sec

itle: US-09-846-456-1 arfect score: 3231

Perfect score: 3231 Sequence: 1 acagggcatggtggcaggtg......gcccacatccccaccactt 3231

Scoring table: IDENTITY\_NUC Gapext 1.0

Searched: 383533 segs, 122816752 residues

Total number of hits satisfying chosen parameters: 76706

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 08
Maximum Match 1008

Maximum Match 100% Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 3, Appli	3	'n	1	12,	20,	21,	22,	20,	21,	22,	7, 8	3,	•	10,	10,	Sequence 43, Appl	43,	17,	4	32		3,		Sequence 67, Appl		Sequence 79, Appl
COLUMN TO THE PARTY OF THE PART	ID	US-09-797-906-3	US-09-797-906-3	US-09-817-180-3	US-09-341-587-7	US-09-078-294-12	US-08-724-394A-20	US-08-724-394A-21	US-08-724-394A-22	US-08-724-394A-20	US-08-724-394A-21	US-08-724-394A-22	US-08-814-095-7	US-09-210-748A-3	US-08-257-963B-10	US-08-367-841A-10	PCT-US95-07201-10	US-08-367-841A-43	PCT-US95-07201-43	US-09-128-155-17	US-09-268-992-7	US-08-975-080-35	US-09-630-706-10	US-09-496-694B-3	US-08-814-095-7	883	8-832-877	US-08-781-891-79
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	Score	278.2	277.2	271.8	269.4	261.6	257.8	257.8	257.8	253	253	253	252.2	251.4	243.4	243.4	243.4	243.4	243.4	243.4	242.4	240.2	240.2	240.2	240	239	239	238.8
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Sequence 2, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 43, Appl	Sequence 43, Appl	Sequence 3, Appli	Sequence 128, App	Sequence 3, Appli	Sequence 17, Appl	Sequence 7, Appli	Seguence 3, Appli	Sequence 12, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 28, Appl	Sequence 59, Appl	Sequence 8, Appli
US-09-103-875-2	US-08-257-963B-10	US-08-367-841A-10	PCT-US95-07201-10	US-08-367-841A-43	PCT-US95-07201-43	US-08-157-171-3	US-09-050-159-128	US-09-210-748A-3	US-09-128-155-17	US-09-341-587-7	US-09-817-180-3	US-09-078-294-12	US-08-618-100B-3	US-08-973-544-1	US-09-564-805-28	US-09-608-285A-59	US-09-608-285A-8
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7.3	7.2	7.2	7.2	7.2	7.2	7.0	7.0	6.9	6.9	6.9	6.8	6.7	9.9	6.5	6.5	6.4	6.4
234.6	232.6	232.6	232.6	232.6	232.6	226	226	223	222.6	221.8	219.8	217.6	211.8	210.4	209.4	206.6	205.4
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## ALIGNMENTS

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APPLICATE: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND TITLE OF INVENTION: USES THEREOF FILE PROTEING HUMAN PROTEASE PROTEINS, AND FILLE OF INVENTION: USES THEREOF FILE REFERENCE: CLOOLISICIP CURRENT APPLICATION NUMBER: US/09/797, 906 CURRENT APPLICATION NUMBER: US/09/797, 906 CURRENT FILING DATE: 2001-03-05 SOFTWARE: FASTSEQ for Windows Version 4.0
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61.5%; Pred. No. 1.1e-58;
tive 0; Mismatches 328;
              Sequence 3, Application US/09797906
Patent No. 6329188
                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (1)...(84495)
OTHER INFORMATION: n = A,T,C or
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Best Local Similarity 61.5
Matches 553; Conservative
                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND TITLE OF INVENTION: USES THEREOF FILE REFRENCE: CLOOlisicip CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT APPLICATION NUMBER: US/09/797,906
SOFTARRE: FastSEQ for Windows Version 4.0
SSOFTARRE: FastSEQ for Windows Version 4.0
LENGTH: 84495
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            35170 ccctagatttaatatgtctacaggaaatacaaggacagagaaacatattaattgacacc 35229
                                                                                                                                   35230 accaagatacaactggtaagttacagaatgtgagaagtgctagggacaaattcattttct 35289
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8.6%; Score 277.2; DB 4;
61.1%; Pred. No. 1.9e-58;
iive 0; Mismatches 338;
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OTHER INFORMATION: n = A,T,C or G
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Patent No. 6329188
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Best Local Similarity 61.1
Matches 556; Conservative
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GENERAL INFORMATION:
APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOI183
CURRENT APPLICATION NUMBER: US/09/817,180
CURRENT FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                   35377 AATAAGGTCTATTGTACTTGATTGCTATGTCTCTTATGCCAGTTTTAATGAATTCCTCCC 35318
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                                                                                                                8.4%; Score 271.8; DB 4; Length 15297; 62.9%; Pred. No. 1.8e-57;
                                                                                                                                            0; Mismatches 287; Indels
         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
                                                                                                                                             Matches 577; Conservative
NUMBER OF SEQ ID NOS: 4
                                                                                                                                Best Local Similarity
                                                               ; ORGANISM: Human
US-09-817-180-3
                                    LENGTH: 15297
                                                  TYPE: DNA
                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.3%; Score 269.4; DB 4; Length 28720; Best Local Similarity 61.5%; Pred. No. 9.7e-57; Matches 589; Conservative 0; Mismatches 296; Indels 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        843 ccaaaacccaatttattgaccaaggttattctttgactgaggcaaggggggtccgc
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APPLICANT: Mollenhauer, Jan
TITLE OF INVEWTION: Protein Containing an SRCR Domain
TILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver: 2.1
                                                                                                                         Sequence 7, Application US/09341587
Patent No. 6346606
                                    Db 15255 ttttaaaaagaatgaag 15271
1258 tttctaagggcaaacag 1274
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                                                                                                           US-09-341-587-7
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1258 TCATTATACATTTGTCCAAATCTACAGAATGTACAACACCAAAGCTTGGGTGATAATGAG 1199

775 aaacaagatgaaacagaggcagaaagactttacgtaaattgctcatcatgtggttgtcaa 834

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955 ttctttttattttcttgacacggagtcttgctctgtcactcaggctggagtgcagtggc 1014

1198 GAGTCAATGTTGGTCCATCAATTGCAACAAAGGTACCACAGTGGTGTAGGATGTGGATAA 1139

835 gtttgaccccaaaacccaatttattgaccaaggttattctttgactgaggcaagggggtc 894

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1075 tcctgag-----ataacaggcgcccgccaccacatctggctaatttttgtatttta 1126

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1127 gtaaagactgggtttcatcatgttggccaggttggtttcgaactcctgacctgaggtgag 1186

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1187 ctgcccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 1244

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                   19399 tttetttetttttttttettetggaeatggagtetegetetgtetegetggaetgtagt 19458
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62.1%; Pred. No. 6.7e-55;
ive 0; Mismatches 309; Indels 31; Gaps
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Sequence 12, 12/21
Patent No. 626521
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILLING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 62.18
Matches 558; Conservative
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845 CIGCCCACTIGGCCTICCAAAGIGCIGGGATIACAGGIGIGGAGCCACCGCGCCTGGC 788
                                                                                                                                                                                                                                                                                                                                            No. 5872237el
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APPLICANT: Ruddy, David A.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Two Embarcadero Center, 8th Floor
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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                                                                                                                        Sequence 20, Application US/08724394A Patent No. 5872237
                                                                                                                                                                                   APPLICANT: Feder, John N. APPLICANT: Kronmal, Gregory S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         San Francisco
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                 US-08-724-394A-20/c
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605 gocatgattggatcactgcactccagcctgggtagacagagcaagaccctgtctcaaaaa 664

1378 AAAAAAAAAAAAAATCAGTGGTTGTGCAGTTAGGAAAAGGGAGAGAGGAGTAAGCAGGTGG 1319

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Db 172474 -AAAAATACAAAAGTTAGCTGGCGTGGTGGCACATGCCTGTAGTCCCAGCTACTGGGGGA 172416
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11.4%; Pred. No. 2.1e-53;
.ve 0; Mismatches 312;
                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                            STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                          Query Match 8.0%;
Best Local Similarity 61.4%;
Matches 545; Conservative
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Db 172523 CAC------GAGGTCAAGACCACCCTAGCCGAAATGGTGAAACCCGTCTCTATT- 172473
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                      Db 171760 CCAAAGTGCTGGGATTACAGGAGTGAGCCACTGCGCCCGGCCCGTT 171714
1204 ccaaagtgctgggattacaggcatgagccactgcgcccagctcagat 1250
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61.4%; Pred. No. 2.1e-53;
ive 0; Mismatches 312;
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                                                                                                                                                       Sequence 21, Application US/08724394A
Patent No. 5872237
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REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
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NDEDNESS: not relevant
LOGY: not relevant
ET TYPE: cDNA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
TRNGTH: 246240 base pairs
                                                                                                                                                                                                                                          Kronmal, Gregory
Lauer, Peter M.
Ruddy, David A.
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N: 536
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NAME: Fitts, Renee A.
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LOCATION: 1..246240
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
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Matches 545; Conserv
                                                                                                                                                                                                 GENERAL INFORMATION:
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Db 172295 ATAATAATAATAATAATAATAATAATAATAATAATTAGGATGCATTTTATCCTATTAATAATATAC 172236
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                                                                                                                                                                        Db 172355 GCCACTGCACTCCAGCCTGGTGACAGAGTGAGACTCCGTCTAAAAATAATAATAATAATA 172296
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556 ggctaaggtgggaggatcgcttgagcccagggagtcaagtctacactgagccatgattgg 615
                                                                                                                 796 gaaagactt----tacgtaaattgctcatcatgtggttgtcaagtttgaccccaaaaccc 851
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                                                                                                                                                                                                                                      TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
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APPLICANT: Feder, John N.
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APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
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STATE:
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D 172474 -AAAAATACAAAATTAGCTGGCGTGGTGGCGCACATGCCTGTAGTCCCAGCTACTGGGGA 172416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 172235 CICITGTCGGTGGTTTTCAGCGACTCTTCAGAGGCCAAAGAGTAAGTTTTCCCTTAGCCC 172176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD 172582 GCCGGGTGCAATGCTCACGCCTGTAATCCCACGCACTTTGGGA-GCTGAGGCGGGCAGAC 172524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD 172523 CAC------GAGGTCAAGACCACCCTAGCCGAAATGGTGAAACCCCGTCTCTAT- 172473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 172355 GCCACTGCACCTGGTGACAGAGTGAGACTCCGTCTAAAAAATAATAATAATAATA 172296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 gccgggcacaatggctaatgcctgtaatcccagcactttgggaggctgaggccagaggat 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 cgcttgagctccagagtttgagaccagcctggataacatggcaaaacctgtctctacaa 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    556 ggctaaggtgggaggatcgcttgagcccagggagtcaagtctacactgagccatgattgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              796 gaaagactt----tacgtaaattgctcatcatgtggttgtcaagtttgaccccaaaaaccc
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                                                                PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 257.8; DB 2;
Pred. No. 2.1e-53;
0; Mismatches 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                              017957-000100
                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179:
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEPAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: not relevant TOPOLOGY: not relevant
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Best Local Similarity 61.4%;
Matches 545; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 246240 base pairs
Floppy disk
                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: not r
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MEDIUM TYPE:
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                                                                   SOFTWARE:
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Db 171938 CAAGCTCCGCCTCCCGGATTCACGCCATTCTCTGCCTCAGCCTCGAGCAGCTGGGAC 171879
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                                                                                                                                                                                                                                                                             taacctctgcctcccgggttcaagcgattctcctgcctcagcctcctga-----gat 1083
                                                                                                                                                                                     aacaggcgcccgccaccacatctggctaatttttttattagtaaagactgggtttca 1143
972 gacacggagtcttgctctgtcactcaggctggagtgcagtggcatgatctcgactcactg 1031
                                                                                                                                                                                                                                                                                                                                                                                                 171760 CCAAAGTGCTGGGATTACAGGAGTGAGCCACTGCGCCCGGTT 171714
                                                                                                                                                                                                                                                                                                                                                                      Oy 1204 ccaaagtgctgggattacaggcatgagccactgcgcccagctcagat 1250
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APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-0CT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Two Embarcadero Center, 8th Floor
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US-08-724-394A-20
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/08724394A Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 01799:
TELEPHONE: 415-576-0200
TELEPHONE: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid STRANDEDNESS: not relevant TOPOLOGY: not relevant
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SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 1..246240
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US-08-724-394A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 171881 CCCAGCTGCTCAGGAGGCTGAGGCAGGAGAATGGCGTGAATCCGGGAGGCGGAGCTTGCA 171940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 172000 AAACAACAACAACAAAAAAACAGGCAGTGATGTTTTATGTGGGTCAGTGTGAAGTAGAGA 172059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172060 TCAAAGGAGAAAACGGCCAATCTTACCAAATAATGGATGCAGAAATAATGTCTCATGGAGA 172119
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                                                                                                                                                                                                                                                                Db 171765 CTGAGGCGGGCCGATCAC--GAGGTCAGGAGATCGAGACCATCCTGGTTAACAAAGTGAA 171822
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                                                                                                     361 aagatgaagaaacaggccgggcacaatggctaatgcctgtaatcccagcactttgggagg 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601 ctgagccatgattggatcactgcactccagcctgggtagacagagcaagacctgtctca
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                                                                                                                                                                                                                                                                                                                       accctgtctctacaaaaaaaaatacaaaaattagatggtggtggtggcatgcacctgtggt
                                                    30;
Length 246240;
                                                    Indels
7.8%; Score 253; DB 2; L
61.5%; Pred. No. 3.2e-52;
tive 0; Mismatches 315;
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Query Match 7.8°
Best Local Similarity 61.5°
Matches 552; Conservative
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STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Ruday, David A.
APPLICANT: Thomas, Minston
APPLICANT: Thomas, Minston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Tra
TITLE OF INVENTION: Sequences an
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-724-394A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 171765 CTGAGGCGGGCCGATCA--GAGGTCAGGAGATCGAGACCATCCTGGTTAACAAAGTGAA 171822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 aagatgaagaaacaggccgggcacaatggctaatgcctgtaatcccagcactttgggagg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 ctgaggccagaggatcgcttgagctccagagtttgagaccagcctggataacatggcaaa 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661 aaaaaaaagaaatgaaagagaaagaaagaaagaaagagagagagagagaggaggagg 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 cccagctacttgggaggctaaggtgggaggatcgcttgagcccagggagtcaagtctaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601 ctgagccatgattggatcactgcactccagcctgggtagacagagcaagaccctgtctca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.8%; Score 253; DB 2; Length 246240; Best Local Similarity 61.5%; Pred. No. 3.2e-52; Matches 552; Conservative 0; Mismatches 315; Indels 30;
                                                                                                  TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
                                                                                                                                                                                               ADDRESSEE: TOWNSEND and TOWNSEND and CREW STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: /note= "HLA-H.CONTIG" US-08-724-394A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35,136
ER: 017957-000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0175
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
                         APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
David A.
                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature rocation: 1..246240
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                       USA
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MOLECULE TYPE:
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COUNTRY:
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Db 172060 TCAAAGGAGAAAACGGCCAATCTTACCAAATAATGGATGCAGAAATAATCTTCATGGAGA 172119
                                                                                                                                                       Db 172120 AGCCACTTTAATTATGTCTTAAATGAGAGTAACAAATTAAACATAAGAACCTGTAGGGGC 172179
                                                                                                                                                                                                                                                                                                           Db 172180 TAAGGGAAAACTTACTCTTTGGCCTCTGAAGAGTCGCTGAAAACCACCGACAAGAGGAAG 172239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 172478 AGAGACGGGGTTTCACCATTTCGGCTAGGGTGGTCTTGACCTCGTGGTCTG------ 172528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 172358 AATCTCGCCTGCAACCTCCGCCTCCCGAGTTCAAGCAATTCTCCTGCCTCAGCCTC 172417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 172418 CCCAGTAGCTGGGACTACAGGCATGTGCCACGCCCAGCTAACTTTTGTATTTTTAAT 172477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              957 ctttttattttttttttgacacggagtcttgctctgtcactcaggctggagtgcagtgcat 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ctgagataacaggcgccgccaccacatctggctaatttttgtatttttagt 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1129 aaagactgggtttcatcatgttggccaggttggtttcgaactcctgacctgaggtgaggt 1188
                                                                               777 acaagatgaaacagaggcagaaagactttacgtaaattgctcatcatgtggttgtcaagt 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 172529 --CCCGCCTCAGCTCCCAAAGTGCTGGGTTACAGGCGTGAGCCATTGCACCCGGCT 172583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy 1189 gcccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagct 1245
                                                                                                                                                                                                                                       837 ttgaccccaaaacccaatttattgaccaaggttattctttgactgaggcaaggggtccg
                                                                                                                                                                                                                                                                                                                                                                                          1017 gatctcgactcactgtaacctctgcctcccgggttcaagcgattctcctgcctcagcctc
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Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOWNSEND and TOWNSEND and CREW LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 171881 CCCAGCTGCTCAGGAGCCTGAGGCAGCAGCAGAGTGGCGTGAATCCGGGAGGCGGAGCTTGCA 171940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 172060 TCAAAGGAGAAAACGGCCAAICTTACCAAATAATGGATGCAGAAATAATCTTCATGGAGA 172119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 172120 AGCCACTTTAATTATGTCTTAAATGAGAGTAACCAATTAAACATAAGAACCTGTAGGGGC 172179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172180 TAAGGGAAAACTTACTCTTTGGCCTCTGAAGAGTCGCTGAAAACCACCGACAAGAGGAAG 172239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D 172300 ATTATATT-TTTAGACGAGTCTCACTCTGTCAC-CAGGCTGGAGTGCAGTGGCGC 172357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 172358 AATCTCGGCTGCTGCAACCTCCGGCTCCGGGTTCAAGCAATTCTCCTGCCTCAGCCTC 172417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 172000 AAACAACAACAACAAAAAAAACAGGCAGTGATGTTTATGTGGGTCAGTGTGAAGTAGAGA 172059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172418 CCCAGTAGCTGGGACTACAGGCATGTGCCACCACGCTAACTTTTGTATTTTAAT 172477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cccagctacttgggaggctaaggtgggaggatcgcttgagcccagggagtcaagtctaca 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                               Length 246240;
                                                                                                                                                                                                                                                                                                                                                                          7.8%; Score 253; DB 2; Length 24
61.5%; Pred. No. 3.2e-52;
tlve 0; Mismatches 315; Indels
                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22
                                                                             LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 61.55
Matches 552; Conservative
                                                                                                                                                  TOPOLOGY: not rele
MOLECULE TYPE: CDNA
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1189 geccaecttggeeteccaaagtgetgggattacaggcatgagecactgegeecaget 1245
Db 172478 AGAGACGGGGTTTCACCATTTCGGCTAGGGTGGTCTTGACCTCGTGGTCTG
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STREET: 30500 No. 6025183thwestern Highway, Suite 410
CITY: Farmington Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTR:.

2 IP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: DEATH PC COMPATIBLE
COMPUTER: PATENT PC TOSA MS-DOS
COMPUTER: PATENT PC TOSA MS-DOSA MS-D
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OCHER INFORMATION: /function= "ACHE Promotor"
OTHER INFORMATION: /standard_name= "ACHE Promotor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function= "(translation start:
24110)"
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DESCRIPTION: /desc = "Cosmid including ACHE
DESCRIPTION: promotor, ACHE gene and ARS gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function= "non-translated"
/gene= "ACHE"
/number= 1
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NAME: Wontgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELERAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7.
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08814095 Patent No. 6025183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 22465..22537
OTHER INFORMATION: /fur
OTHER INFORMATION: /ger
OTHER INFORMATION: /num
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
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OTHER INFORMATION: /number= 7

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LOCATION: complement (34528..34895)
OTHER INFORMATION: /function= "arsenite resistance OTHER INFORMATION: gene" "AFR"
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 1
                                                                                                                                                                                                                                                                        OTHER INFORMATION: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /gene= "ACHE" ATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: 28008..28129
IDENTIFICATION METHOD: experimental
OCHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 6
                                                                                  NAME/KEY: exon
LOCATION: 25524..26009
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene="ACHE"
OTHER INFORMATION: /number= 3
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NAME/KEY:
CACATION: 27255..28007
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 5
/evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 2
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LOCATION: complement (34092..34358)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
FEATURE:
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
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LOCATION: complement (33297..33408)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 5
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RMATION: /gene= "AR"
RMATION: /number= 6
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LOCATION: complement (32569..32628)
OTHER INFORMATION: /gene="AR"
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LOCATION: 27005..27274
IDENTIFICATION METHOD:
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27385..27387
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LOCATION: 28129..28131
INFORMATION:
INFORMATION:
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OTHER INFORMATION:
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NAME/KEY:
LOCATION:
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LOCATION:
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Db 14835 CCTTTTTTAAGTTACATTTGGGCCAGGCACAGTGGCTCATGCCTTTAATCCTGTACTT 14776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONTION: COMPLEMENT (29664..29856);
COTHER INFORMATION: /gene="ARS"
COTHER INFORMATION: /number= 16
US-08-814-095-7
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OTHER INFORMATION: /number= 15
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LOCATION: compl
NAME/KEY: exon
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LOCATION: comp.
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                                                                                                                                                                                                                                                                                                                               5662 gagctgagattgtgccactacactccagcctgggtgacaagagcgaaactccgtctcaaa 5721
                                                                                                  5422 atctggccgggcatggtggcttatgcctataatttcagcactttggaaggctgaggcagg 5481
                                                                                                                                                                                                                                                  371 aacaggeegggeacaatggetaatgeetgtaateeeageaetttgggaggetgaggeeag 430
                                                                                                                                           aggategettgagetecagagtttgagaecageetggataaeatggeaaaaecetgtete 490
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61.0%; Pred. No. 1.5e-52;
live 0; Mismatches 286; Indels
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    Best Local Similarity 61.09
Matches 575; Conservative
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                                    14296 CTGAATCCATGTTTTTACATAATTGTAGCATCCTTTACACACTCTTCTGTACTTGACTTA 14237
                                                                                                                              14476 AAATTGAAAACGTATAAAGTGAAAAGTTCTCCTCTTCCCTGCCTTCCTCGACCCAGTATT 14417
                                                                                                                                                                                                              14236 AAAAAAAAAAAAAAAAACCTAGCTAACAGTGTATCTTAAGGATAGTTCCAGATTTGTACA 14177
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                                                                                                                                                                                                                                                                                                                                                                                                                        ggcaagggggtccgctctcctgggccttggggctttagaaagctcatctctggcctttctg 942
      1062 tectgeeteageete-----etgagataacaggegeeegecacatetggetaat
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                                                                                          ----acagaggcagaaagactttacgtaaattgctcat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hermeking, Heiko
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
FILE REFERENCE: 1107.77810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.8%; Score 251.4;
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PRIOR APPLICATION NUMBER: 60/069,416
PRIOR FILING DATE: 1997-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13876 CCACACCTGGCCCTCATTCTTTTTT 13848
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SOFTWARE: FastSEQ for Windows Version 3.0
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' > 0.48-10
' Sequence 10, Application US/08257963B
' Patent No. 5840686
' GENERAL TANGE
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TYPE: DNA ORGANISM: Homo sapiens

US-09-210-748A-3

Query Match

LENGTH: 7680

SEQ ID NO 3

US-09-210-748A-3

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APPLICANT: Chader, Gerald J.; Becerra, S.
APPLICANT: Particia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
TITLE OF INVENTION: BLOLOGICLA ACTIVITY AND SEQUENCES ENCODING
TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
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OTHER INFORMATION: Derived from human placental genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US1
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,963B
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD:
                                                                                                                                      NUMBER OF SEQUENCES: 4. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: DASH II
                                                                                                                                                                                                                                          New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                               10154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                          STATE:
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tctgtcactcaggctggagtgcagtggcatgatctcgactcactgtaacctctgcctcc 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1099 ccacatctggctaatt---tttgtatttttagtaaagactgggtttcatcatgttggcca 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1156 ggttggtttcgaactcctgacctgaggtgagctgcccaccttggcctcccaaagtgctgg 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6284 GGCTGGTCTCGAACTCCTGACCTCAGGTGATCCCCCGGCCTCGGTCTCCCCAAAGTGCTGG 6343
                                                                                                                                                                                                                 5879 CATTGACCTAAG--------5914
                                                                                                                                                                                                                                                                                                  5915 TATATATCACTTAGGGACAAAACTTACATGGTAAAAGTAAAAGAAATGTACGAAAATA 5974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gggttcaagcgattctcctgcctcagcctc-----ctgagataacaggcgcccgcca 1098
567 gaggatcgcttgagcccagggagtcaagtctacactgagccatgattggatcactgcact 626
                                                                                 807 cgtaaattgctcatcatgtggttgtcaagtttgaccccaaaacccaatttattgaccaag 866
                                                                                                                                                                                                                                                                                                                                                                                                                                  867 gttattctttgactgaggcaagggggtccgctctcctgggccttgggctttagaaagctc 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      747 ggaaggaaaaaagatgaaaaaagaaaaaaaaaaaaagatgaaaaggcagaaagacttta
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Patent No. 6319687

GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Tombran-Tink, Joyce
ITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1216 gattacaggcatgagccactgcgcccagctcagat 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
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345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: Floppy Disk
IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
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5760 GAGAACCICTIGAACCCGGGAAGCGGAGGTIGCAGTGAGCCGACATIGCACCCTGCACT 5819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 ggaagacagaatatacatcttctctccattttaaagatgaagaaacaggccgggcacaat 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gaggatcgcttgagcccagggagtcaagtctacactgagccatgattggatcactgcact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.5%; Score 243.4; DB 4; Length 7210; Best Local Similarity 60.9%; Pred. No. 1.4e-50; Matches 569; Conservative 0; Mismatches 276; Indels 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD:
OTHER INFORMATION: 7.0 kb No. 6319687 1-No. 6319687
OTHER INFORMATION: fragment; Derived from human placental
OTHER INFORMATION: genomic DNA; also referred to as JT106
                                                                                                                                                                                                                          REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US2
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 758-4800
TELEFRAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7210 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
                               APPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                               NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: DASH II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: JT6A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-367-841A-10
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ggttggtttcgaactcctgacctgaggtgagctgcccaccttggcctcccaagtgctgg 1215
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5915 TATATATCACTTAGGGACAAAAACTTACATGGTAAAAGTAAAAAGAAATGTACGAAAATA 5974
                                                                                        -----GAACTGAGGCGGAAATATAAGGTTGTCA 6043
                      807 cgtaaattgctcatcatgtggttgtcaagtttgaccccaaaacccaatttattgaccaag 866
                                                                 867 gttattctttgactgaggcaagggggtccgctctcctgggccttgggctttagaaagctc 926
                                            5975 ATAAAAATCAAATTCAAGATGGTGGTTATGGTGACGGGAAA-
                                                                                                                                                                                                                                                                                                                                                           1216 gattacaggcatgagccactgcgcccagctcagat 1250
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Search completed: September 20, 2002, 03:21:22 Job time: 14171 sec

7;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

September 19, 2002, 23:20:20; Search time 3895 Seconds (without alignments) 11196.062 Million cell updates/sec Run on:

US-09-846-456-1 3231 1 acagggcatggtggcaggtg.....gccccacatccccaccatt 3231 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

13736207 seqs, 6748477542 residues Searched:

27472414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:\* Database :

gb\_est2:\*
gb\_htc:\*
gb\_gss:\*
em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_vrt:\* 1: em\_estba:\*
2: em\_esthum:\*
3: em\_estin:\*
4: em\_estin:\*
5: em\_estov:\*
6: em\_estpl:\*
7: em\_estro:\*
8: em\_tc:\* gb\_est1:\* 9: 10: 11: 12:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AU121731 AU121731				A0265389 CITBI-E1-	A0418551 RPCI-11-2	A0475181 CITBI-E1-	A0347610 RPC111-12	AW023111 df49d08.v	AG075934 Pan trod	B50449 CIT-HSP-422	AQ537948 RPCI-11-3	AI754653 cr28c08.x	AQ200209 RPCI11-45	AV755654 AV755654	AO314669 RPC111-10	AQ414845 RPCI-11-2
SUMMARIES	ID	AU121731	AW748338	AU135588	AW816516	AQ265389	AQ418551	AQ475181	AQ347610	AW023111	AG075934	B50449	AQ537948	AI754653	AQ200209	AV755654	AQ314669	AQ414845
	DB	6	6	6	σ	12	12	12	12	σ	12	12	12	σ	12	σ	12	12
	Query Match Length DB	763	289	736	457	577	544	719	581	338	999	493	622	514	739	827	484	487
фP	Query	10.4	7.4	6.9	9.9	6.8	6.8	6.7	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9
	Score	336	237.8	221.8	221.2	219.4	218.6	215.2	214.2	213.4	213.4	213.2	213.2	213	213	213	212.8	212.8
	ult No.	Н	7	m	4	Ŋ	9	7	æ	6	10	11	12	13	14	15	16	17
	Result No.		υ		O	O		O	U	O			υ		ပ	O	υ	υ

AQ040260 CIT-HSP-2 AW341978 hb74d10.*	A0634562 RPCI-11-4		A0587429 CITBI-E1-	AW973181 EST385279	AQ387027 RPCI11-15	BG682030 602629995	AL524675 AL524675	AI733856 zo19c03.v	AW069227 cr41h09.x	AA644090 ab62b04.s	AQ412598 RPCI-11-1	AG102895 Pan troql	BG697612 602660853	A0221138 HS 2258 B	AV719392 AV719392	AW973187 EST385285	AG050562 Pan trodl	AG036967 Pan trodl	B65075 CIT-HSP-201	B59854 CIT-HSP-345	BG697217 602660451	AI275982 gw06h11.x	AQ426532 CITBI-E1-			BF854308 MR2-EN009
2 AQ040260 AW341978		9 AW970571		Ø	12 AQ387027		-	_		~	12 AQ412598			12 AQ2211:38	AV719392	AW973187			2 B65075	12 B59854		K	2 AQ426532	2 AQ554309	11 AF119908	0 BF854308
501 1		521 9									605 1			•	577 9	541 9				642 1			0		0	624 1
9.9	9.9	9.9	9.9	6.5			6.5		6.5		6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5
212.4	212.2	212.2	212	211.4	211.4	211.2	211	210.8	210.6	210.6	210.6	210.4	210.2	210	210	209.8	209.8	209.6	209.4	209.4	209.4	209	209	209	209	208.8
18	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

linear EST 19-OCT-2000 WAl000851 5', mRNA	Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. ., Ishii,S., Saito,K., Kawai,Y., :amura,Y., Nagai,T., Sugano,S. and		ss sequencing: Helix n: Department of rersity of Tokyo, and	3 others
AU121731 AU121731 MAMMA1 Homo sapiens cDNA clone MAMMA1000851 5', mRNA sequence. AU121731 AU121731 GI:10936966	ens : Metazoa; Chordata; Eutheria; Primates; I to 763) !shikawa,T., Suzuki,Y	Jacobart Takao Isogai Contact: Takao Isogai Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-488-52-3951 Fax: 81-488-52-3952	HAIL INDIAN DIVIDECT, 3" - & 3"-end one pass sequencing: He.  Wirology, Institute of Medical Science, University of Tokyo, Helix Research Institute.  Location/Qualifiers  Location/Qualifiers  Location/Qualifiers  //Organism="Homo sapiens" //do_xref="taxon:9606" //clone="MAMMA1000851" //clone="MAMMA1000851" //clone_lib="MAMMA1000851" //clone_lib="mammary gland" //note="Vector: pwR18SF13"	4
RESULT 1 AU121731 LOCUS DEFINITION ACCESSION VERSION V	ALTHORS SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL COMMENT	FEATURES	BASE COUNT ORIGIN

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1 (bases 1 to 289)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOilveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-2704922
Fax: +55-11-270001
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6st2=RC6-BT0252-271099-012-c108t3=1999-10-27st4=1)
Seq primer: puc 18 forward
High quality sequence start: 146
High quality sequence stop: 289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW748338 28-APR-2000 RGG-BT0252-271099-012-c10 BT0252 Homo sapiens CDNA, mRNA sequence.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                              2956 gggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggcgc 3015
                                                                                                                                                                                                                                                                                                             3016 tttgctccttgttttttccccggttctgttttctccccttctccggaaggcttgtcaagg 3075
                                                                                                                                                                                                                                                                                                                                                                                                             3076 ggtaggagaaagaggaagcaaacacaaaagtggaaaacaggtaagaggctctccagtgact 3135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3136 tacttgggggttattgttttgtttcgaggccaaggaggcttcgggaagtgctcggtttcg 3195
                                                                                                                 61 GGGCTGCGGCAGGGCAGGGCGGGGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGCCC 120
                                                                                                                                                                                                                                                                                                                                          121 TTGCTCCTGTTTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCCGAAGGCTTGTAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                       241 TACTTGGGCGTTATTGTTTTGTTTCGAGGCCAAGGAGGCTTCGGGAAGTGCTCGGTTTCG 300
                                                                   Gaps
                                                                                                                                                               1 AATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
               Length 763;
                         DB 9;
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10.0%; Bred. No. >...
100.0%; Pred. No. >...
0; Mismatches
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/clone_lib="BT0252"
/dev_stage="Adult"
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                                      Best Local Similarity 100.0
Matches 336; Conservative
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/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue many and cona applification were performed under low
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 736)
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                                                                                                                                                                                                                                                           2006 gctgcacttcacaaatgtatacaaactaaatacaagtcctgtgtttttatcacagggagg 2065
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/clone="pLACE1002437"
/clone_lib="PLACE1"
/tissue_type="placenta"
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70 c 51 q 7
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Contact: Takao Isogai
Genomics Laboratory
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases to 457)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

'M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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This sagnescondludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV0-ST0236-171
299-075-bl2&t3=1999-12-17&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 457.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                2894 gtaattgcgagcgaggtgagtgagtggggccgggacccgcagagccgacccttctctc 2953
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                                                                          Length 736;
  others
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                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
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Pred. No. 6.8e-20;
0; Mismatches 2
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170
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/db_xref="taxon:9606"
/clone_lib="ST0236"
/dev_stage="Adult"
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Matches 223; Conservative
199
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AQ265389 577 bp DNA linear GSS 27-OCT-1998 CITBI-E1-2509010.TF CITBI-E1 Homo sapiens genomic clone 2509010,
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Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
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Clones are available from Research Genetics (info@resgen.com). BAC
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K. Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 955 ttcttttttatttttcttgacacggagtcttgctctgtcactcaggctggagtgcagtggc 1014
                                                                                                                                                                                                                                                                                      tcctga----gataacaggogccgccacacatctggctaattttgtatttttag 1127
                                                                                                                                                                                                                                                                                                                                                                                                                     337 TCCTGAGTATCTGGACTACATGCACACCACCACCACCTGGCTAATTTTTGTATTTTTAG 278
                                                                                                                                                                                                                                            457 ITTITITITITITITITGAGACAGAGTCTTGCTCTGCCTCCCAGGCTGGAGTACAGTGGC 398
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Other GSSs: CITBI-E1-2509010.TR
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
                                                                                                                                                      38;
                                                                                                            Score 221.2; DB 9;
Pred. No. 1e-19;
low stringency conditions."
95 c 115 g 90 t
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/clone_lib="CITBI-E1"
/sex="male"
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/db_xref="GDB:7577811"
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AQ475181/c
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Homo sapiens genomic clone RPCI-11-203K4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    library availability, please contact Pieter de Jong Pieterde de Jong Pieterdedjong, med. buffalo. edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.seq primer: SP6 class: BAC ends.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 544)
 /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
calrech Human BAC Library D"
1 127 c 137 g 146 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                         1128 taaagactgggtttcatcatgttggccaggttggtttcgaactcctgacctgaggtgagc 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1016 tgatctcgactcactgtaacctctgcctcccgggttcaagcgattctcctgcctcagcct 1075
                                                                                                                                                                                                                                                                                                                                                         1076 cctga----gataacaggcgcccgccaccactctggctaatttttgtatttttag 1127
                                                                                                                                                                                                                                                                                                      370 CGATCTCGGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGTGATTCTCCTGCCTCAGCCT 311
                                                                                                                                                                                                                                                                                                                                                                               250 TAGAGACGGGGTTTCACCATGTTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGGCGATC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1248 gatccatccctttctaagggcaaacagtccatggtgcaaaggggccatgccacccagag 1306
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Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                       8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 GAGATACATTTTTGTAAATCTAGACTGGAGTCAGTGGACAGCTCCTCAGGCAAAGGGAG 72
                                                                                                                                    DB 12; Length 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotko Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850
                                                                                                                                Score 219.4; DB 12; Length
Pred. No. 1.6e-19;
0; Mismatches 71; Indels
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Other_GSSs: RPCI-11-203K4.TV
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AQ418551
AQ418551.1 GI:4476275
                                                                                                                                  Query Match 6.8%;
Best Local Similarity 78.0%;
Matches 280; Conservative
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/organism="Homo sapiens"

source

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Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from Callech Libraries for Sequence-Ready
Map Building
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 719)
                                                                                                     EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                               ttgggaggctgaggccagaggatcgcttgagctccagagtttgagaccagcctggataac 472
                                                                                                                                                                                                                                                                                                                                                                                                                     533 cctgtggtcccagctacttgggaggctaaggtgggaggatcgcttgagcccagggagtca 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
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Pred. No. 2e-19;
0; Mismatches 125; Indels 3;
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Other_GSSs: CITBL-E1-2589B9.TR
Other_GSSs: CITBL-E1-2589B9.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
                                                                                                                                                1 others
                                                                         /cel_type="Lymphocytes"
//cel_type="Lymphocytes"
//note="Vector: pBACe3.6; Site_1:
RPCIII Human Male BAC Library"
R c 165 q 85 t
                 /clone="RPCI-11-203K4"
/clone_lib="RPCI-11"
/sex="Male"
/db_xref="taxon:9606"
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Best Local Similarity 70.5%;
Matches 306; Conservative 0
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RPCI11-126022.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-126022,
DNA sequence.
                                                                                                                                                                                                                                                                                                      ij
           Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                         http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 581)
                                                                                                                                                                                 /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
Calrech Human BAC Library D"
1 162 c 180 g 149 t
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                                                                                                                                                                                                                                                                                                     83; Indels
                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                    Location/Qualifiers
1. 719
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                           /clone="2589B9"
/clone_lib="CITBI-E1"
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Other_GSSs: RPCI11-126022.TV
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                                                                                                                                                                    /sex="male"
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Fax: 301 838 0208
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df4908.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486822 5', mRNA sequence.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 338)
Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R.
                                                                                                                                                                          library availability, please contact Pieter de Jong prehased from topieter/dedjong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: SP6 class: BAC ends.
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
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Clones are derived from the human BAC library RPCI-11. For BAC
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Similarity 81.2%; Pred. No. 7.4e-19;
Contact: Shaying Zhao, William Nierman, Mark Adams
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                                                                  9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                       Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="RPCI-11-126022"
/clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 264; Conservative
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AG075934.1 GI:16627736
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-068P19.R.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                       To bases 1 to 666)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totchi, Y., Watanabe, H. and Sakaki, Y.
Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@sc:riken.go.jp/, URL:http://hgp.gsc:riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347 ttctctccattttaaagatgaagaaacaggccgggcacaatggctaatgcctgtaatccc 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 TGCTTTCTTTAAGAAACCAGTGGAGGTGAGCTGAGCACAGTGGCTTACACTTGTAATCCC 140
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Fullyman.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totocki,Y., Mattanabbe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 213.4; DB 12; Length
Pred. No. 8.8e-19;
0; Mismatches 136; Indels
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R.Site 1 : SacI
R.Site 2 : SacI.
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Best Local Similarity 69.78;
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                                                                                                                                                                                                                                                                         REFERENCE
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SOURCE
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/db_xref='taxon:9606"
/clone='InMogres_146882"
/clone='InMogres_Petal Cochlea"
/tissue_type="cochlea"
/tissue_type="cochlea"
/dev_stage="lfo_22 week fetus"
/dev_
and Morton,C.C.
Isolation of novel and known genes from a human fetal cochlear cDNA
library using subtractive hybridization and differential screening
Genomics 23, 42-50 (1994)
95130111
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                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov).
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@imago.llnl.gov) for further information. Plate: LLAM6188 row: G column: 15
Seq primer: MISRPI reverse primer (ABI).
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Pan troglodytes DNA, clone: PTB-068P19.R, genomic survey sequence.
                                                                                                                                                                                                                       Reproductive Biology
Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
Tel: 617 738 6996
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8
                                                                                                                                                                                            Departments of Pathology and Obstetrics, Gynecology and
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                                                                                                                                                                                                                                                                                                                                                                                      Email: ccmorton@bics.bwh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                               Contact: Morton, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ದ
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                                                                                                                                                                                      DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ung@ash.tree.caltech.edu
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                        Kim, U.-J., Adams, M.D. and Simon, M.I.
Determination of clone end sequences of human Bacterial Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: T7
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Gaps
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Division of Biology, MS 147-75, Pasadena, CA 91125,
Tel: 626 796 706
Fax: 626 395 4901
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                                                         499 AAAAGAAAAGAAAGGAAGAAGAAGAAAGA 533
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/organism="Homo sapiens"
/db_xref="GDB:5393148"
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Other_GSSs: CIT-HSP-422022.TP
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CalTech Genome Research Lab
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 622)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hbe@tigr.org
Clones are derived from the human BAC_library RPCI-11. For BAC
272 CICAGGIGACCCCCCCCCCCCCCCCCCAAATGCTGGGATTACAGGTGTGAGCCACCG 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
                                                                                 1237 egeceageteagatecatecetttetaagggeaa 1270
                                                                                                                332 CGCCCGGCCCTCAGCCTTCAAATGACAA 365
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/clone="RRCI-11-323E19"
/clone="RRCI-11"
/sex="Male"
/cell_type="Lymphocytes"
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A1754653.1 GI:5132917
EST.
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Beckstrom-Sternberg, S.M., Green, E.D., Powell, J.I., Yang, L.M., Robey, P.G., Hotchkiss, R.N. and Francomano, C.A.
SGAP: The Skeletal Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI; mRNA made from human bone marrow stroma, cDNA made by oligo-dT priming. Directionally cloned. Size-selected for exerge insert size >0.5 kb. Library supplied by Dr. Libin
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 514)
954 tttetttttatttttettgacaeggagtettgetetgteaeteaggetggagtgeagtgg 1013
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                                                   601 ctgagccatgattggatcactgcactccagcctgggtagacagagcaagaccctgtctca 660
                                                                         8; Gaps
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Plate: 28 row: c column: 08
Seq primer: -21Al3 forward primer (ABI).
Location/Qualifiers
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10/100101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
TEL: 301-402-4977
Fax: 301-496-7157
                                                                                                                                                                                      6.6%; Score 213; DB 9; Length 514;
81.8%; Pred. No. 1.1e-18;
tive 0; Mismatches 50; Indels
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/sex="mixed"
/tissue_type="bone marrow stroma"
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/db_xref="taxon:9606"
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139 c 1
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Matches 261; Conservative
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Other_GSSs: RPCIII-4503.TK
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(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1074 ctcctga-----gataacaggcgcccgccaccactctggctaatttttgtattttt 1125
                                                                                                                               1126 agtaaagactgggtttcatcatgttggccaggttggtttcgaactcctgacctgaggtga 1185
                                                                                                                                                                                                                                                                     /sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
RPCI11 Human Male 9 170 t
                                                                   134 CTCCTGAGTAGCTGGGATTACAGGCGCGCCACCACCCCGGCTAATTTTTGTATTTTT 193
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Clones are derived from the human BAC library RPCI-11. For BAC
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/clone_lib="RPCI-11"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 827)

8 Gu,J., Zhao,M., Huang,O., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., S Gu,J., Li,N., Oian,B., Liu,F., Ou,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gao,G., Wang,Z., Zhang,O., Chen,S., Han,Z. and Chen,Z. Thomo sapiens CDNA BM clones

NT Upublished (2000)

Contact: Zequang Ham

Chinese National Human Genome Center at Shanghai

51 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

7el: 86-21-50801919(ex.45)

Fax: 86-21-50801919

Email: hanzgechgc.sh.cn

This clone is available at CHGC in Shanghai.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                      OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No. Score Match Length DB, ID

Description

AX351030 Sequence AV25548 Homo sapi AX09289 Sequence AV25277 Homo sapi AL35368 Human DNA AC012230 Homo sapi AC021345 Homo sapi AC021345 Homo sapi AC061345 Homo sapi AX06013 Sequence AX06013 Sequence AX060719 Sequence AX060719 Sequence AX060719 Sequence AX060719 Sequence AX060719 Sequence AX060719 Sequence AX137513 Sequence AX13751 Sequence AX13764 Sequence AX13764 Sequence AX13764 Sequence AX13764 Sequence AX13764 Mus muscu AX05294 Sequence AX13713 Sequence AX13713 Sequence AX13713 Sequence AX13713 Sequence AX351035 Sequence AX13713 Sequence AX13714 Homo sapi AX052347 Homo sapi AX13713 Sequence AX13714 Homo sapi AX13714 Homo sapi	AXOB/114 Mus muscu ACOR7114 Mus muscu ACOZ5794 Mus muscu ACOZ5794 Mus muscu ACO11558 Homo sapi ACO10427 Mus muscu AL603913 Mus muscu	6. DNA linear PAT 06-FEB-2002 raniata; Vertebrata; Euteleostomi; atarrhin1; Hominidae; Homo. Lemoine,C., Naudin,L., Denefle,P., A. and Santamarina Fojo,S. 001; s"
357 6 AX351030 334 9 AE275548 399 6 AX092589 480 9 HSA252277 6064 2 AC012230 6144 9 AE287262 6209 2 AC012230 6442 6 AX060892 6442 6 AX060892 6442 6 AX060892 6444 6 AX060892 6474 6 AX060892 6474 6 AX060893 6474 6 AX060893 6474 6 AX127764 6 AX127764 6 AX139817 6 AX139817 6 AX139817 6 AX139817 6 AX139818 6 6 AX135918 6 6 AX1351035 6 6 AX351035	000000000000000000000000000000000000000	357 bp (018374 cata; C tes; C tes; C 's, C.', cequenc '-NoV-2 ers sapien 9606"
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Santamarina-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A., Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E., Francois,T.L. and Brewer,H.B. Jr.
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Submitted (08-JUN-2000) Molecular Disease Branch, National
Institutes of Heath, National Heart, Lung and Blood Institute,
Bethesda, MD 20892, USA
Location/Qualifiers
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Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
20345099
                       Length 357;
100.0%; Score 357; DB 6; Length 3
100.0%; Pred. No. 2e-98;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18399)
Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M.
Compositions and methods for modulating hdl cholesterol and tridlyceride levels
Patent: WO 0115676-A 1 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)
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                                                                                                                                                                                                                                 DB 9;
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Sequence 1 from Patent W00115676.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
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human ATP-binding Cassette
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                                                                                                                                                                                                                                                                                                        function="cholesterol efflux regulatory proteiin"
   tggaaggtctcagctgagagggctggattagcagtcctcattggtgtatggctttgcagca
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Porsch-Oezcueruemez,M.K.
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/gene="ABC-1"
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSRROT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP database can be found at
                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL353685 129608 bp DNA linear PRI 01-JUN-2001
Human DNA sequence from clone RP11-31J20 on chromosome 9, complete
sequence.
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RP11-31J20 is from the library RPCI-11.1 constructed by the group
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
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on Jun 8, 2001 this sequence version replaced gi:14272260.
                                                                                                                                                                                                                                                                                            61 ataactgatggctgtttcccctcctgctttatctttcagttaatgaccagccacgggcgt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 TTCAGAAGAAGACAAACAGTAAGCTTGGGTTTTTCAGCAGCGGGGGGTTCTCTCATTTTT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttcagaagaagacaaacagtaagcttgggtttttcagcagcggggggttctctcatttt
                                                                                                                                                                                                                                                  150 ATAACTGATGGCTGTTTCCCCTCCTGCTTTATCTTTCAGTTAATGACCAGCCAC-GGCGT
                                                 ij
Length 480;
                                                    Indels
  DB 9;
  Score 340.2; DB 9
Pred. No. 2.9e-93;
0; Mismatches 3
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98.9%;
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AL353685.23
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Best Local Similarity
Matches 353; Conserv
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IMPORTANT: This sequence is not the entire insert of clone RP11-31J20 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-31J20 is at 129608 in this sequence. The true right end of clone RP11-413C10 is at 2000 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="L1MB8 repeat: matches 6040. .6173 of consensus"
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//orde="L2 repeat: matches 2137. .2750 of consensus"
24245. ... 24544
//orde="Alusg repeat: matches 2. .302 of consensus"
24556. ... 24587
//orde="8" copies 4 mer acac 96% conserved"
//orde="2504. .26561
//orde="250504" copies 2 mer ta 69% conserved"
26849. ... 26892.
//oce="11" copies 4 mer tata 81% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2777. .2896
/note="MIR repeat: matches 6. .128 of consensus"
3237. .3415
/note="LIME repeat: matches 5696. .5821 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L2 repeat: matches 2649. .2698 of consensus" 2496. .2714 //note="Mar repeat: matches 12. .250 of consensus" 2777. .2896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12145. .12713

//note="L2 repeat: matches 1363. .1940 of consensus"

13890. .13969

/note="L2 repeat: matches 2611. .2701 of consensus"

15380. .15411

/note="16 copies 2 mer ac 87% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5522. 6818
Morte="Allog repeat: matches 1. .295 of consensus"
7282. 7415
                                                                                                                                                                                                                                                                                                                                              1358. .1653

Anote-"Alusc repeat: matches 1. .288 of consensus"

1828. .1877
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16868. .17049
17049. .1829
/note-"Alusg repeat: matches 1. .287 of consensus"
1829. .18553
/note-"Alusg repeat: matches 1. .293 of consensus"
20310. .20616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Alusc repeat: matches 1. .298 of consensus"
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27998. .28103
/note="MIR repeat: matches 28. .145 of consensus"
28515. .28626
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of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                clone_lib-"RPCI-11.1"
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                       /clone="RP11-31J20"
                                                                                                                                                                                                                                                                                     /chromosome="9"
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/note="L1MD2 repeat: matches 5774. .6331 of consensus" 40256. .40534
/note="L2 repeat: matches 2256. .2533 of consensus"
                                                                                                                                                                           // Josephson 2000 Amer atgg 79% conserved" 34435...34588 Anote="Merson repeat: matches 13...189 of consensus" 34729...34873 Anote="Mir repeat: matches 49...198 of consensus" 36802...35951 Anote="Mir repeat: matches 77...248 of consensus" 37.004e="2.009ies 39 mer 92% conserved" 37613...37980
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/note="LiMA9 repeat: matches 5893. .6307 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSq repeat: matches 145. .313 of consensus"
49097. .49181
                                                                                    Anote-"WERSA repeat: matches 60. .188 of consensus" 32450. .32536
Anote-"WERSA repeat: matches 14. .106 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="IrR16A repeat: matches 6. .450 of consensus" 45359. .45486
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/hote="L2 repeat: matches 2565. .2710 of consensus"
57406. .57567
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49578, .49758
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54337. .54544
                   31424. .31734
/note="AluSp repeat: matches 1. .308 of consensus"
31987. .32116
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSc repeat: matches 1. .308 of consensus" 39674. .40243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 9. .188 of consensus" 49847. 49873 //note="MIR repeat: matches 155. .182 of consensus" 4974. 50188 /note="AluJb repeat: matches 3. .311 of consensus" 50189. 50347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L2 repeat: matches 2088. .2723 of consensus"
60201. .60355
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[7915. .48083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54337. .54344
/note="MIR repeat: matches 25. .246 of consensus"
54754. .55032
/note="AluSp repeat: matches 1. .302 of consensus"
55042. .55343
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19443. .60004
/note="AluSg repeat: matches 1. .302 of consensus"
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/note="MIR repeat: matches 49. .234 of consensus"
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66027. .56232
//note="MIR repeat: matches 21. .259 of consensus"
66233. .56286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 1. .139 of consensus" 46654. 46693. 46693 47118. .47429
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51677. .51977
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/note="MIR repeat: matches 20. .183 of consensus"

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Diren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baltren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Borkhylan, J., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Bouslavkiy, L., Boukhgalter, B., Borown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrin, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
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Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175064)
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                                                                                                                                                                                                                                                                                /note="MER5A repeat: matches 72. .186 of consensus" 66825. .67131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat: matches 78. .243 of consensus" 64590. .64653
/note="32 copies 2 mer ta 70% conserved" 64593. .64656
/note="16 copies 4 mer atat 68% conserved" 64981. .65042
/note="MERSA repeat: matches 15. .72 of consensus"
                                                                                                                                                                                                    65043. .65341
/note="Alusx repeat: matches 1. .299 of consensus"
65342. .65441
                                                                                                                                                                                                                                                                                                                                      /note="AluSx repeat: matches 1. .306 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                   95.3%; Score 340.2; DB 9 98.9%; Pred. No. 7.2e-93; iive 0; Mismatches 3
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AC012230.3 GI:7637254
HTG; HTGS_PHASE1; HTGS_DRAFT.
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Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 22, 2000 this sequence version replaced gi:6454033. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                            Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zlmmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: 12510
Center clone name: 1_M_10
Center clone name: 1_M_10
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 117571 bases at least Q40
Consensus quality: 145749 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; sum-of-contigs
Quality coverage: 3.2 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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7879: contig of 1994 bp in length
797: gap of 100 bp
9686: contig of 1707 bp in length
9786: gap of 100 bp
12253: contig of 2467 bp in length
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25707; contig of 3020 bp in length
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f 1270 bp in length
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28184: contig of 2377 bp in length
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3054 bp in length
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38318: contig of 3919 bp in length
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31338: cont
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9687
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20232
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103017 103116; gap of 100 bp 103117 103178; contig of 6062 bp in length 109179 109279 109278; gap of 100 bp 109279 117308; contig of 6052 bp in length 117308 117408 124079; contig of 6672 bp in length 124080 124179; gap of 100 bp 124180 124180 121281; contig of 672 bp in length 131282 131381; gap of 100 bp 131382 131381; gap of 100 bp 131382 13381; gap of 100 bp 131382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13382 13
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                          48216: gap of 100 bp
52618: contig of 4402 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76988: gap of 100 bp 82113: contig of 5125 bp in length 82213: gap of 100 bp 88220: contig of 6007 bp in length
                                                                                          52718: gap of 100 bp
56592: contig of 3874 bp in length
                                                                                                                                                          p of 100 bp contig of 2943 bp in length
                                                                                                                                                                                                                       35: gap of 100 bp 63661: contig of 3926 bp in length
                                                                                                                                                                                                                                                                                                                                                p of 100 bp contig of 2921 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                   58: gap of 100 bp 76888: contig of 5330 bp in length
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103016: contig of 5015 bp in length
                                                                                                                                                                                                                                                                                       o of 100 bp
contig of 4676 bp in length
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1. .1003
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.note="assembly_fragment"

5886. .7879

.note="assembly_fragment"

7980. .9686
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48116: contig of
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                                                                                                                                                    092; gap of
59635; con+
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71458: 7
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82113: con+
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97901; cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 151451 ATAACTGATGGCTGTTTCCCCTCCTGCTTTATCTTTCAGTTAATGACCAGCCAC-GGCGT 151393
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 20114)
Qiu,Y., Cavelier,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F.
Human and mouse abcal comparative sequencing and transgenesis studies revealing novel regulatory sequences
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                                /note="assembly_fragment"
34400. 38318
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71559. .76888
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MEDLINE REFERENCE

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.04328,117287. .117379,
.25424,125754. .125870,
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QQLDGLDWTAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRTISRFMECVNLN
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NKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVVEQAIIRVLTGTEKKTGVYMQQMPY
PCYVDDIFLRVMSRSMPLFWTLAWIYSVAVIIKGIVYEKEARLKETMRIMGLDNSILW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFVFLSVFAVVTLQCFLISTLF
SRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFASLLSPVAFGFGCECFALFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP
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SWSDMRQEVMFLTNVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALF
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                                                                                                7 (bases 1 to 201144)
Olu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submitsed (13-JUL-2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="ATP-binding cassette 1 sub-family A member 1" 33931. .181457
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148575,
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    201144
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Genomics 73 (1), 66-76 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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gene exon

exon

CDS

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.138381 /gene="ABCAl' /number=17

Fri

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Dipublished

State (Dases 1 to 90698)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldain, J., Barna, N., Beckerly, R., Beda, F., Badushin, J., Barna, N., Beckerly, R., Beda, F., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Donlins, M., Doyle, M., Galagan, J., Ferreira, P., Fitzhiup, M., Dorres, C., Gage, D., Galagan, J., Ferreira, P., Fitzhiup, M., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McDwan, P., McGurk, A., McRenan, K., Macdonald, P., Marquis, N., McDwan, P., McCheck, R., McKenan, K., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Storamanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Saquence version replaced gi:6705761.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                            Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90698)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This record contains 92 individual

* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L4483
Center clone name: 24_J_9
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of 905 bp in length
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of 851 bp in length
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f 883 bp in length
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911 1010: gap of 100 bp
011 1873: contig of 863 bp in length
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f 914 bp in length
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f 843 bp in length
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of 878 bp in length
                                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-24J9
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4816: contig of
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1874 1973: gap of
1974 2824: COI
                    AC021345
AC021345.2 GI:9130845
                                                    HTG; HTGS_PHASE0
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                                                                                                                                                                                                          Unpublished
                                                                              human.
  DEFINITION
                                                                                              ORGANISM
                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                              REFERENCE
AUTHORS
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                      ACCESSION
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KEYWORDS
SOURCE
                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
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Pred. No. 7.7e-93;
0; Mismatches 3
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145441. .145513
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Matches 353; Conservative
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38402: contig of 880 bp in length
38502: gap of 100 bp
39480: contig of 878 bp in length
39480: gap of 100 bp
8755: contig of 908 bp in lengtn
5: gap of 100 bp
9753: contig of 898 bp in length
33: gap of 100 bp
10757: contig of 904 bp in length
                                                                                                                                                                                                                                                                                                                                                                           19732: gap of 100 bp
20634: contig of 902 bp in length
20734: gap of 100 bp
21620: contig of 886 bp in length
21720: gap of 100 bp
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16677: contig of 915 bp in length
17: man of 100 bp
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                                                                                10758 10857; gap of 100 bp
10858 11732; contig of 875 bp in length
11733 11832; gap of 100 bp
11833 12739; contig of 907 bp in length
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13710: contig of 871 bp in length
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15662: contig of 878 bp in length
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17678: contig of 901 bp in length
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22568: contig of 889 bp in length
23668; gap of 100 bp
24554: contig of 886 bp in length
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32452: contig of 899 bp in length
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13811 14684: contig of 874 bp in length
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28466: contig of 902 bp in length
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30447: contig of 883 bp in length
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31453: contig of 906 bp in length
53: gap of 100 bp
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3347: contig of 895 bp in length
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contig of 894 bp in length
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43357: contig of 858 bp in length
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64006: contry
126: gap of 10v - 10v - 65015: contig of 889 bp in 65115: gap of 100 bp 100 b
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68048 68934: contig of 887 bp in length
6935 69034: gap of 100 bp
69035 69910: contig of 876 bp in length
69911 70010: gap of 100 bp
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10 of 100 pp 1111 contig of 904 bp 1111 contig of 904 pp 1111 contig of 909 pp 1111 contig of 909 pp 1111 contig of 90 pp 1111 contig of 909 contig of 900 contig of 90
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Pred. No. 1.3e-65;
0; Mismatches 4
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contig of 880 bp
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contig of 897 bp
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PAT 22-JAN-2001
                               Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10442)

Lawn, R.M., Rade, D. and Garvin, M.

Regulation with binding cassette transporter protein abcl

Patent: WO 0078972-A 128-DEC-2000;

CV THERAPEUTICS, INC. (US)

Location/Qualifiers
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Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abcl polypeptides Patent; Wo 0070871-A 1 28-DEC-2000; CV THERAPEUTICS, INC. (US)
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Best Local Similarity 81.8%; Pred. No. 1.2e-37;
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/organism="Homo sapiens"
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Homo sapiens ATP binding cassette transporter 1 (ABCA1) gene, exon
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                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Blochem. Biophys. Res. Commun. 271 (2000) In press
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aoutzerat, B.E., Fielding, C.J. and Kane, J.P.
                               Db 12931 TTCAGAAGAAGACAAACGTTGGGTTTTTCAAGCGGGGGGTTTTT 12879
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/chromosome="9"
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Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA, complete cds. AF285167.1 GI:9755158
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ARLFSDARRLLLYSOKDTSMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYH
NLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP
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AVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYILGKDIRSEMSTIR
ONLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVGLPSSKLKSKT
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protein_id-"AARP9175.1"
/db_xref="GI:9755159"
/translation-"MACWPQLRLLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRL
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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ABCAl gene expression and apoA-I-mediated cholesterol efflux are
regulated by LXR
                                                                                       217 ttgctgctgtggaagaacctcactttcagaagaagaagacaaacagtaagcttgggtttttca 276
                                                                                                                                            255 CCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTGGCCTCAGCTGAGG 314
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Lawn, Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
Porter, J.G., Seilhamer, J.J., Vaughan, A.M. and Oram, J.F.
Direct Submission
                                                                                                                                                                                                                                                                                                                                   375 GTGGCCTGGCTCTATTTATCTTCCTGATCCTGATCTTTGG 419
                                                                                                                                                                                                                                                                              277 gcagcggggggttctctcttttttttgtggttttgagttggg 321
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/organism="Homo sapiens"
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/cell_type="fibroblast"
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/chromosome="9"
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TITLE
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SOURCE

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GWKLTQQQFYALLWKRLLIARRSKRGFFAQIVLPAVFYCIALYFSLIVPPFGKYPSLE
LQPWMYNEQYTFVSNDAPEDTGTLELLMALTKDPGFGTRCMEGNPIPDTPCQAGEEEW
TTAPYPQTIMULEQUEGNGNWTWONPSPROCESSBKIKKMLDVCPPGAGGLPPPQRKONTA
DILQDLTGRNISDYLWKTYQIIARSLKNK WWNERRYGGFSLGVSWTQALPPEQNKONTA
DIIKQMKKHIKLAKDSSADRPLNSLGREWTGLDTRNNVKVWFNNKGWHAISSFLNVIN
DAIKQMKKHIKLAKDSSADRPLNSLGREWTGLDTRNNVKVWFNNKGWHAISSFLNVIN
NAILRANLQKGERNSHYGTTAFNHPLINLTGQOLSEYALMTTSPVDLVSICVIFMSFV
PASFVVFLQERVSKAKHLQFISGKPVYTRQDLSFYNDNKUFUSUSUSYA
TFVLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDWVKNQAMADALERFGENRFVS
PLSMLCHOVRNLFRANVEGYVFFLITYLLQYREPRRPWAKLSFENDREBGDYRERRQ
RILDGGGONDILETKELTK TRRKRRPANDRISCHELLGGVNGAGKSSTFKM
LTGGOTTVTRGDAFLLKNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGV
PREWCKVGEMAIRKLGLYKYGEKYAGNYSGGNKRKLSTAMALIGGRPVVFLDEFTG
MDPKARRFLWNCALSVVKGGRSVVLTSHRAMECFALLTGREHVERFTG
NREGDGTTIVVRIAGSNPDLKRVQDFFGLAFTRAMINGYQLPSSLSSHARI
FILLGGGGNTTIVVRIAGSNPDLKRVQDFFGLAFTRAMINGYQLPSSLSSHARI
FILLGGGGYTTIVVRIAGSNPDLKRVQDFFGLAFTRAMINVGRPRCLGSVQHLK
NREGDGTTIVVRIAGSNPDLKRVQDFFGLAFTRAMINVQRPRCLGSSLSHRI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10474)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 cccgagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgagg 216
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Regulation with binding cassette transporter protein abc1
Patent: WO 0078972-5 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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Pred. No. 1.2e-37;
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/db_xref="taxon:9606"
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Best Local Similarity 81.8%;
Matches 184; Conservative
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Lawn, R.M., Wade, D. and Garvin, M.
Eawn, R.M., Wade, D. and Garvin, M.
Pagulation with Binding cassette transporter protein abcl Patent: WO 0078972-A 9 28-DEC-2000; CV THERAPEUTICS, INC. (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
217 ttgctgctgtggaagaacctcactttcagaagaagacaaacagtaagcttgggttttca 276
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Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
Atp binding cassette transporter protein abcl polypeptides
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81.8%; Pred. No. 1.2e-37;
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/db_xref="taxon:9606"
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AX060898
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Matches 184; Conservative
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                                                                                                                                                     Query Match 44.6%; Score 159.4; DB 6; Length Best Local Similarity 81.8%; Pred. No. 1.2e-37; Matches 184; Conservative 0; Mismatches 41; Indels
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Patent: WO 0078971-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                        1736436 seqs, 858457221 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                    - nucleic search, using sw model
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AAF24702
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AAC69132
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Maximum DB seq length: 200000000
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Match Length DB
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AAF93082
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AAI62954
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AAC69389
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AAK72952
AAI62955
AAI62956
                                                      AAC69388
AAF83826
                                                                  AAF92835
AAC69387
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                                                                                                                                                                                                                                                                    AAF92831 standard; DNA; 183999 BP
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2000US-0213958.
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WO200115676-A2.
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15-MAR-2000; 23-JUN-2000; 2
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ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
                                                                                                                         diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABCl expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiovascular disease; coronary artery disease; coronary restenosis; cerebrovascular disease; peripheral vascular disease; Alzhelmer's disease; Nomann-Pick disease; Huntington's disease; X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prophylaxis; drug screening; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 53130 tggaggtctcagctgagagggctggattagcagtcctcattggtgtatggctttgcagca 53189
(HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity -
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                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 183999
                                                                                                              The present invention relates to a method for treating a patient
                                                                                                                                                                                                                                                                                                                                                       Human ABC1 gene exon 1 (promoter).
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                                                                         Claim 8; Fig 1; 317pp; English.
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Best Local Similarity 98.93
Matches 353; Conservative
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The invention relates to the human ABC1 cholesterol transporter protein (338082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transporte, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is cocated on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency (FMA). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FMA is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, coronary restencess, and peripheral vascular disease.

Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention promprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease compunials the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also tendencesses compounds which mind ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds of increased risk for cardiovascular disease, desease due to polymorphisms in the increased risk for cardiovascular disease, especially coronary artery disease, or prevent cardiovascular disease, especially coronary artery disease, or prevent cardiovascular disease, especially coronary artery disease, deservascular disease, especially coronary artery disease, decreament of diseases associated disease, Human ABC1 proteins and nucleotides can be used to treat current or prevent cardiovascular disease, especially especially such as Alzhelmer's disease, which according activity, such as Alzhelmer's disease, with ABC1 globogical activity, such as Alzhelmer's disease, and nucleotides proteins wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention specifically excludes proteins with the exact amino acid sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic acid with the exact sequence as Genbank Accession No: AJ012376.1. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence represents the human ABC1 gene promoter region (exon 1).
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                                                                                                                                                                                                                                                                                                                                                              New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.3%; Score 340.2; DB 21; Length 10545; 98.9%; Pred. No. 9.5e-95; ive 0; Mismatches 3; Indels 1; 0
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                                                                                                                                                                                                                                                                    Hayden MR, Wilson AR, Pimstone SN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 50; Fig 12; 229pp; English.
                                                                                                                                                                                                                      (XENO-) XENON BIORESEARCH INC
                                                                                                                                                                                              (UYBR-) UNIV BRITISH COLUMBIA
                    15-MAR-2000; 2000WO-IB00532.
                                                                   99US-0124702.
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Best Local Similarity 98.9
Matches 353; Conservative
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                                                                                            08-JUN-1999;
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are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.

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The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) I polypeptide. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9422-9431. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for
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                                                                                                           8162 ccctgctgtgagctctggccgctgccttccagggctcccgagccacacgctggggggtgct 8221
                                                ggctgagggaacatggcatgttggcctcagctgaggttgctgctgtggaagaacctcact 240
                                                                                                Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9q22-9q31; heart disease; hypercholesterolemia;
                                                                                                                                                           Nucleotide sequence of a human ABC1 polypeptide.
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291..7076
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81.8%; Pred. No. 9.3e-39;
iive 0; Mismatches 41; Indels 0;
                                      Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;
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                                                                                         Best Local Similarity
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             The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) I polypeptide. ABC1 resides in cell membranes and utilises ATP hydrollysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is adfective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q.22-9q.31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated
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                                                                                                                                                                                                                                                                                                                                                                             44.6%; Score 159.4; DB 22; Length ilarity 81.8%; Pred. No. 9.3e-39; Conservative 0; Mismatches 41; Indels
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The present sequence encodes a human adenosine triphosphate (ATP)

binding cassette protein (ABC) 1 polypeptide, and is isolated from
a Tangler disease patient. ABC1 resides in cell membranes and utilises
ATP hydrolysis to transport a wide variety of substrates across the
plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
mobilisation of intracellular cholesterol stores. ABC1 is defective in
Tangler disease, a genetic disorder characterised by abnormal
HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
of 9422-9431. The ABC1 genes and proteins are useful for developing
pharmaceutical agents for the treatment of heart disease and other
disorders associated with hypercholesterolemia and atherosclerosis. The
genes are useful for developing screening assays to screen for compounds
that regulate the expression of genes associated with cholesterol
transport. The genes and proteins are also useful
as diagnostic indicators of cardiovascular disease and other disorders
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(CVTH-) CV THERAPEUTICS INC.
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binding cassette protein (ABC) loplypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises a Tangier disease patient. ABC1 resides in cell membranes and utilises. ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 942-9431. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolems and atherosclerosis. The genes are useful for developing screening assays to screen for compounds transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
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/product= "defective ABC1 polypeptide"
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99US-0153872.
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                                                                                     WO200078972-A2
                                                                                                                                                                                                                                                                                                                                                18-JUN-1999;
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19-NOV-1999;
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ö cccgagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgagg 216 cagttaatgaccagccacggggggtcctgctgtcagctctggccgctgccttccagggct 156 217 ttgctgctgtggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttca 276 Gaps 44.6%; Score 159.4; DB 22; Length 10474; 81.8%; Pred. No. 9.3e-39; tive 0; Mismatches 41; Indels 0; C 277 gcagcgggggttctctctttttttttgagtttggg 321 184; Conservative Best Local Similarity Query Match Matches 97 157 287 407 qq ŏ g δ ò qq δλ g

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AAF24707 standard; DNA; 10474 BP
                                                     AAF24707;
            AAF24707
RESULT
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The present sequence encodes a human adenosine triphosphate (ATP)

binding cassette protein (ABC) 1 polypeptide, and is isolated from
a Tangier disease patient. ABC1 resides in cell membranes and utilises
ATP hydrolysis to transport a wide variety of substrates across the
plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
mobilisation of intracellular cholesterol stores. ABC1 is defective in
Tangier disease, a genetic disorder characterised by abnormal
HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
(9422-9431. The ABC1 genes and proteins are useful for developing
pharmaceutical agents for the treatment of heart disease and other
disorders associated with hypercholesterolemia and atherosclerosis. The
genes are useful for developing screening assays to screen for compounds
transport. The genes and proteins are also useful
transport. The genes and proteins are also useful
as disponsition indicators of cardiovascular disease and other disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 cagitaaigaccagccacggggggcgiccigctgicagcictggccgcigccitccagggci 156
                                                            Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                         Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 10474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "defective ABC1 polypeptide"
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81.8%; Pred. No. 9.3e-39;
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                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 323..7108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-2000; 2000WO-US16591
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20-APR-2001 (first entry)
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Matches 184; Conservative
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19-NOV-1999;
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Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

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binding cassette protein (ABC) I polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in rangler disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterolemia and atherosclerosis. The transport. The genes and proteins are also useful for are also useful assignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
ttgctgctgtggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttca 276
                  Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                                                                                                                                                                                                                                                                                                                                 Human; adenosine triphosphate binding cassette protein 1; ABC1; apoliopprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a human adenosine triphosphate (ATP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product- "defective ABC1 polypeptide"
                                                                   277 gcagcggggggttctctctttttttttgtggttttgagttggg 321
                                                                                                      407 gtggcctggcctctatttatcttcctgatcctgatctctgttcgg 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 30; Page 165-172; 211pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
323..7108
                                                                                                                                                                                             AAF24708 standard; DNA; 10474 BP.
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99US-0153872.
99US-0166573.
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P-PSDB; AAB31367.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis
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19-NOV-1999;
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                                                                                                                                                                                                                                AAF24708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brewer HB;
                                                                                                           97 cagitaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggct 156
                                                                               cagitaaigaccagccacgggcgiccigcigigagciciggccgcigccticcagggci 286
                                                                                                                                                                  ttgctgctgtggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttca 276
                                                                                                                                                                                               347 ttgctgctgtggaagaacctcactttcagaagaagacaaacatgtcagctgttactggaa 406
                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human ABC1 protein, amino acids 1 to 60"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol; cardiovascular; neurological; Tangier disease;, LCAT deficiency; lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
DB 22; Length 10474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is M, Arnould-Reguigne I, Prades C,
Jaye M, Searfoss GH, Remaley A, B
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                            Indels
                                                                                                                                                                                                                        gcagcgggggttctctcttttttttttgtggttttgagttggg 321
                                                                                                                                                                                                                                          407 gtggcctggcctctatttatcttcctgatcctgatctctgttcgg 451
Score 159.4; DB 22;
Pred. No. 9.3e-39;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atherosclerosis, malaria and diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                               Partial human ABC1 cDNA sequence.
                                                                                                                                                                                                                                                                                                                           AAS04035 standard; cDNA; 446 BP.
 44.68;
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Duverger N, Jaye
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                             Matches 184; Conservative
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                 Local Similarity
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Lemoine C,
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  Query Match
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transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological
                                                                                                                                                                                                                                                                             157 cccgagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgagg 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 ttgctgctgtggaagaacctcactttcagaagaagacaaacatgtcagctgctgctggaa 268
                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                              pathologies, and other diseases e.g. Tangier disease, lecithin-
cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                                      40.8%; Score 145.8; DB 22; Length 446;
80.9%; Pred. No. 3.7e-35;
1ive 0; Mismatches 42; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 gcagcgggggttctctcttttttttttgtggttttgagttggg 321
                                                                                                                                                  Seguence 446 BP; 96 A; 123 C; 112 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ABCAl homologue-encoding cDNA, SEQ ID NO:976.
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27-APR-2000; 2000US-0560875.
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Matches 182; Conservative
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P-PSDB; ABB11956.
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conditions, naivour-hands of producing conditions, and sequences ABA08225-ABA09374 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides of the invention. Although novel, many of the bind to polypeptides of the invention. Although novel, many of the colling to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence to prefer that therapeutic applications. The polypeptides of the invention may have various activities; sem cell growth factor activity; hamomodulatory activity; tissue growth activity; immunomodulatory activity; activity crimhibin-related activities; chemotactic or chemokinetic activities; hamomostatic, thrombotic or thrombotytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Comparisons, eq., by protein or gene therapy, such conditions include cancers, haematopoletic disorders (e.g., mayloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), conditions, eq., by protein or gene therapy. Such conditions and some cancers, haematopoletic disorders (e.g., mayloid or lymphoid cell disorders), cronic inflammatory conditions (e.g., asthma or arthritis), cronic inflammatory conditions (e.g., asthma or arthritis), arterial ischemia, bone disorders (e.g., coronary heart disease, arterial ischemia, bone disorders (e.g., oronary heart disease, arterial ischemia, bone disorders (e.g., oronary heart disease, arterial ischemia, bone disorders (e.g., oronary heart disease, arterial and enterial and burns, incisions and ulcers), while those with comming and ulcers), while those with the immunomodulatory activities may be used in the treatment of viral, and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides with growth factor activity may be used in cell cultures to promote cell growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                      Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 cccgagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgagg 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                 treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                    Human proteins and DNA encoding sequences useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 7086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.8%; Score 145.8; DB 22;
80.9%; Pred. No. 1.3e-34;
Live 0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 833-835; 1963pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.9
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
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AAK52667 standard; cDNA; 7086 BP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, itsue growth factor activity, immunomodulatory activity and activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                       cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the sequence listing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 cagitaaigaccagccac-ggcgiccigctgigagciciggccgcigcciccagggci 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 ttgctgctgtggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttca 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 cccgagccacacqctggggggggctgacggggaacatggcttgttggcctcagctgagg 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                   vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cccgagccacacgctgggcgtgctgagggaacatggcatgttggcctcagctgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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Zhang J, Ren F, Chen R, Wang ZW;
F, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 7086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAM80020) are omitted as the relevant pages from were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.8%; Score 145.8; DB 2.80.9%; Pred. No. 1.3e-34; ive 0; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 4558-4560; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful in diagnosis and gene therapy -
                                                  Human polynucleotide SEQ ID NO 2196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C, Drmanac RT,
Wang D, Wang J, Zh
Yang Y, Wejhrman T,
                                                                                                                                                                                                                                                                                                                                  2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0663561.
                                                                                                                                                                                                                                                                                 05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                  2000US-0496914
                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-2000; 2000US-0728422
                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-476283/51.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                        Human; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAM79534
                                                                                                                                                                                                            WO200157190-A2.
                                                                                                                                                                                                                                                                                                                                  27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammation
                06-NOV-2001
                                                                                                                                                                                                                                                                                                                    03-FEB-2000;
                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157
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Human; ATP binding cassette transporter 1; ABC1; coronary heart disease; dermatological; atheroscalerosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to four common polymorphisms in the gene encoding ATP-binding cassette transporter-1 (ABC1). ABC1 is associated with decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in ABC1 directly affects cellular lipid homeostasis, which is a key factor in the atherogenetic processes. The ABC1 polymorphisms are useful for diagnosing and treating lipid disorders, cardiovascular diseases (coronary heart disease, atherosclerosis) and inflammatory diseases (psoriasis, lupus erythematosus). The identification of ABC1 as a transporter for interleukin-lobeta (IL-lobeta) identifies this gene as a candidate for treatment of inflammatory diseases including rheumatold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 ttgctgctgtggaagaacctcactttcagaagaagacaaacatgtcagctgctgctggaa 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New adenosine triphosphate binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 7260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other
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                                                                                                                                       388 gtggcctggcctctatttatcttcctgatcctgatctctgttcgg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ATP binding cassette transporter 1 (ABC1) gene.
                                                                     277 gcagcggggggttctctctttttttttgtggttttgagttggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.8%; Score 145.8; DB 22;
80.9%; Pred. No. 1.3e-34;
ive 0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Human ABC1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 321..7106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 1; 48pp; English.
                                                                                                                                                                                                                                                                                                                       AAD21326 standard; DNA; 7260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-2000; 2000EP-0105820.
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Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JAN-2002
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The present sequence is that of cDNA encoding the human adenosine triphosphate (ATP) binding cassette transporter I (ABCI) protein (See AAMSO227). The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AA.T/0314, using an alternative ATG codon as initiation codon and thereby adding an
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= b
/note= "alternative open reading frame of AAI70314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New adenosine triphosphate binding cassette transporter gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                                         ATP binding cassette transporter 1; ABC1; human; lipid disorder; cholesterol; cardiovascular disease; inflammatory disease; antiinflammatory; antilipaemic; antipsoriatic; dermatological; rangier disease; coronary heart disease; diagnosis; gene therapy;
                                                                                                  277 gcagcggggggttctctctttttttttgtggttttgagttggg 321
                                                                                                                            405 gtggcctggcctctatttatcttcctgatcctgatctctgttcgg 449
                                                                                                                                                                                                                                                                    Human ATP binding cassette transporter 1 (ABC1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 26-28; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                         AAI70315 standard; cDNA; 7260 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replace(2969,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replace(1516,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replace(3836,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replace(976, A)
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                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-640389/74.
                                                                                                                                                                                                                                                                                                                                                polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAM50228
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1136554-A1
                                                                                                                                                                                                                                            07-JAN-2002
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                                                                                                                                                                                                                    AAI70315;
                                                                                                                                                                    RESULT 13
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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
extra 40 N-terminal amino acids to the encoded ABC1 protein (see AAM50228). The invention provides 4 common polymorphisms in the dalagener. These were identified by sequencing the ABC1 gene in different rangier kindreds. In the variant genes (numbering as in AI70314), G is changed to A at position 596, T is changed to C at position 1136, A is changed to G at position 2589 or G is changed to C at position 136, or any combination of these. All of these polymorphisms alter the amino acid sequence of ABC1 and therefore polymorphisms alter the amino acid sequence of ABC1 and therefore may affect its function. The 2 most common polymorphisms (G596A) and A2899G) are both associated with a decreased in vitro ApoA-1 mediated efflux of cholesterol from mononuclear phagocytes, a cature typical of Tangier disease. 3 of the variants (G596A, A289G and G3456C) are significantly increased in a population of established coronary heart disease (CHD) relative to CHD-free control subjects. The use of the provided ABC1 polymorphisms for the diagnosis and treatment of lipid disorders, cardiovascular diseases, and inflammatory diseases (e.g. psoriasis, lupus erythematodes) is claimed. Modulation of ABC1 transcripts or proteins by antisense or ribozyme technology or RNA decoys is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 cagttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggct 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 ttgctgctgtggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttca 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 tigcigcigiggaagaaccicactitcagaagaagacaaacatgicagcigitaciggaa 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 cagitaatgaccagccac-ggcgtccctgctgtgagctctggccgctgccttccagggct 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 7260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.8%; Score 145.8; DB 22; Length
80.9%; Pred. No. 1.3e-34;
Live 0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 giggectiggectetatitatetteetgateetgatetetgitegg 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK51683 standard; cDNA; 7281 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0560875.
2000US-0598075.
2000US-0620325.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157190-A2
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20-JUN-2000;
19-JUL-2000;
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                                                                                                                                      Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 cagttaatgaccagccacggcgtccctgctgtcagctctggccgctgccttccagggct 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 cccgagccacacgctggggggggctgaggggaacatggcttgttggcctcagctgagg 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ttgctgctgtggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttca 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol; cardiovascular; neurological; Tangier disease;, LCAT deficiency; lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
                                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                      Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 cccgagccacacgctgggggggggggggggggaacatggcatgttggcctcagctgagg
                                                                                                                                                   Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.8%; Score 145.8; DB 22; Length 7281; 80.9%; Pred. No. 1.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;
                                                                                                                          Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wa Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 gcagcgggggttctctctcttttttttgtggttttgagttggg 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.3e-34;
0; Mismatches 42;
                                                                                                                                                                                                                                                                                                        Claim 1; Page 1086-1096; 6221pp; English.
                                                                                                                                                                                                                                                                        useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS06120 standard; cDNA; 9741 BP
                  15-SEP-2000; 2000US-0663561.
20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
 01-SEP-2000; 2000US-0654936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ABC1 DNA sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 80.9
Matches 182; Conservative
                                                                                                                                                                                                  WPI; 2001-476283/51.
                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                       P-PSDB; AAM78550.
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The sequence represents the coding sequence #1 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing ardiovascular and neurological pathologies, and other diseases e.g. Tangler disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                                                                                                                                              Naudin L;
                                                                                                                                                                                                                                                                                                            Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L
Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 cagttaatgaccagccac-ggcgtccctgctgtgagctctggccgctgccttccagggct 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 ttgctgctgtggaagaacctcactttcagaagaagacaaacagtaagcttgggttttca 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                    New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtggcctggcctctatttatcttcctgatcctgatctctgttcgg 313
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                                                       /*tag= a
/product= "Human ABC1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 204-208; 368pp; English.
                 Location/Qualifiers
185..6967
                                                                                                                                                                                                                    26-OCT-1999; 99EP-0402668.
01-MAR-2000; 2000US-0186260.
                                                                                                                                                                               26-OCT-2000; 2000WO-EP10886.
                                                                                                                                                                                                                                                                       (AVET ) AVENTIS PHARMA SA.
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-316327/33.
P-PSDB; AAU02176.
                                                                                                         WO200130848-A2.
                                                                                                                                                                                                                  26-OCT-1999;
                                                                                                                                               03-MAY-2001
                                                                                                                                                                                                                                                                                                          Denefle P,
Lemoine C,
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September 20, 2002, 03:21:22; Search time 110.16 Seconds (without alignments) 796.035 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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357
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database

Issued\_Patents\_NA:\*

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/cgn2\_6/ptodata/2/ina/pcTUS\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/pcTUS\_cOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			dР			SUMMARIES	
Result No.	1t.	Score	Query	Query Match Length	DB	ID	Description
	-	31	8.7	10968	~	US-08-680-327-2	Sequence 2, Appli
	7	31	8.7	10968	4	US-09-228-246-1	Ä
O	m	30.8	٠.	1037	Н	US-08-462-195-3	m
ပ	4	30.8	8.6	1037	7	US-08-636-883-3	m
ပ	2	30.8	8.6	1037	m	US-09-127-829-3	e,
ပ	9	30.4	8.5	2473	4	US-09-173-914-3	'n
	7	30	8.4	686	4	US-08-988-321B-37	37,
	8	30	8.4	989	4	US-08-397-220B-25	25,
	6	30	8.4	4771	~	US-08-866-650-2	Sequence 2, Appli
	10	30	8.4	4771	7	US-09-021-287-2	7
	11	30	8.4	4771	4	US-09-240-473-2	7
υ	12	30	8.4	5143	Н	US-08-574-043A-7	7,
O	13	30	8.4	5143	7	US-08-795-015-7	7
	14	30	8.4	7881	7	US-08-751-189-1	'n
	15	30	8.4	7881	7	US-09-060-836-1	٦,
	16	30	8.4	7881	4	US-09-184-445-1	'n
	17	30	8.4	33529	4	US-09-144-085-3	'n
ပ	18	29.6	8.3	424	П	US-08-609-657-15	15,
ပ	19	29.4	8.2	2480	4	US-09-534-638-3	Sequence 3, Appli
	20	29.4	8.2	3147	~	US-08-781-802-7	7
	21	29.4		3147	4	US-08-694-078-7	7,
	22	29.4		3147	4	US-09-058-260-7	Sequence 7, Appli
	23	29.4	8.2	31491	4	US-09-360-186-1	'n
	24		٠	573	~	US-08-290-665A-124	124
Ü	25	29.5	8.2	573	Ŋ	PCT-US95-10398-124	Sequence 124, App
	26		•	2892	7	US-08-264-534-5	ď
υ	27	29.5	8.2	2892	-	US-08-083-590A-1	1,

Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 7, Appli
US-08-465-500-5 US-08-346-126-5 US-08-3346-128-5 US-08-537-384-1 US-08-640-906-1 US-08-640-906-1 US-09-39-936-1 US-09-39-36-1 US-09-39-36-1 US-08-525-058A-7 US-08-525-058A-7 US-08-525-058A-7 US-08-525-058A-7 US-08-525-058A-7 US-08-384-616-7 US-08-38-904-668A-7 US-08-290-665A-115
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28992 28992 28992 28992 28992 28992 3647 3647 3647 3457 3455 3455 3455
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## ALIGNMENTS

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ADDRESSEE: Klarquist Sparkman Campbell Leigh & ADDRESSEE: Whinston
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MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IDN PC compatible
COMPUTER: IDN PC compatible
OPERATING SYSTEM: MS DGS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NAMER: US/08/680,327
FILING DATE: July 11, 1996
CLASSIFICATION DATA:
APPLICATION NAMER: 0800
PRIOR APPLICATION NAME: 0800
FILING DATE: September 22, 1994
CLASSIFICATION: 000
FILING DATE: APPLIAN: 13, 1994
CLASSIFICATION NUMBER: 08/227,360
FILING DATE: APPLIAN: 13, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 5151-45038
TELECOMMUNICATION INFORMATION:
TELEFHONE: (503) 226-7391

**TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10968 base pairs
                                                                                                                                                                                                                                                STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
STREET: Portland
STATE: Oregon
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
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US-08-680-327-2
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CORRESPONDENCE ADDRESS
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US-08-636-883-3/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
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                                                                                                                                                      DD 10808 AGAAGATGAACCTGCACTAATTAATCCTCCCTTTATGAATAAGAGAATGAGAAAAAAGATG 10867
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                                                                                                                              209 agctgaggttgctgctgtggaagaacctcactttcagaagaagaagacaaacagtaagcttgg 268
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                                                                                        Gaps
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                                                                                                                                                                                                                                              Db 10868 GAGCTTCATGAAGACCAAAAGTTACCTTTTTTTTTTTTAATGGCATTACTTTG 10918
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                                        DB 2; Length 10968;
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Staskawicz, B. S. et al.
TITLE OF INVENTION: PRF Protein and Nucleic Acid Sequences: C
TITLE OF INVENTION: and Methods for Plant Pathogen Resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.7%; Score 31; DB 4; Length 10968; 55.0%; Pred. No. 6.2; tive 0; Mismatches 50; Indels
                                                                                   50; Indels
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                                      Query Match
8.7%; Score 31; DB 2
Best Local Similarity 55.0%; Pred. No. 6.2;
Matches 61; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 51700
CURRENT APPLICATION NUMBER: U$/09/228,246
CURRENT FILING DATE: 1999-01-11
EARLIER APPLICATION NUMBER: 08/680,327
EARLIER APPLICATION NUMBER: 08/310,912
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1994-09-22
EARLIER FILING DATE: 1994-09-22
EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09228246 Patent No. 6245510
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Patent No. 5789544
GENERAL INFORMATION:
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APPLICANT: SATTO, IZUMU
APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: HONDA, YOSHIKAZU
APPLICANT: SEKI, MAKOTO
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Matches 61; Conservative
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LOCATION: (8300)..(9466)

US-09-228-246-1
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LOCATION: (3879)..(8186)
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US-09-228-246-1
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107 ccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctcccgagccac 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 acgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttgctgctgt 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1037;
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30.8; DB 1; Length 1 Pred. No. 2.1; 0; Mismatches 117; Indels
                               ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/462,195
FILING DATE: 05-UN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 gttctctcatttttttttgtggttttgagttggggat 324
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                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/08/446,303
FILING DATE: 22-MAY-1995
APPLICATION NUMBER: US 08/074,584
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: US 08/074,584
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5789544man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 413-3000
TELEFRAX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
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Best Local Similarity 46.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
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                                                                                                       STATE: Virginia COUNTRY: U.S.A.
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227 ggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttcagcagcggggg 286
                                                                    117 ACTCCACCAACGATCTGACCACCGCCCGGGAACTTAACGTCCTGTGGGCGGCGGTTGGTG 58
                                                                                                                                     287 gttctctcatttttctttgtggttttgagttggggat 324
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APPLICATION NUMBER: US 08/074,584

FILING DATE: 11-JUN-1993

APPLICATION NUMBER: JP 152487/1992

FILING DATE: 11-JUN-1993

ATTONNEY/AGENT INFORMATION:

NAME: Oblon, NO. 6063904man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 4169-003-0

TELECOMUNICATION INFORMATION:

TOTAL T
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/446,303
                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09127829
Patent No. 6063904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MIYANURA, TATSUO
APPLICANT: SATTO, IZUMU
APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: SEKI, MAKOTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
17..1036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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; LOCATION:
US-09-127-829-3
                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-127-829-3/c
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                                                                                      APPLICANT: MITAMORA, TATSUO
APPLICANT: MITAMORA, TATSUO
APPLICANT: MATSUORA, YOSHINARU
APPLICANT: MATSUORA, YOSHINARU
APPLICANT: HONDA, YOSHINAZU
APPLICANT: HONDA, YOSHINAZU
APPLICANT: SEKI, MAKOTO
TITLE OF INVENTION: METHOD FOR PRODUCING ECTOPROTEIN OF
TITLE OF INVENTION: HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Allington
STREET: VITGING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/636,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: US 08/074,584
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: UP 152487/1992
FILING DATE: 11-JUN-1992
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: ODLON, NO. 5830691man F.
RGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 4169-003-0
TELECOMMUNICATION INFORMATION:
FELEPHONE: (703) 413-3000
TELEFAX: (703) 413-3200
TELEFAX: (703) 413-220
TELEFAX: (703) 413-200
TELEFAX: (703) 413-200
TELEFAX: (703) 413-200
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/446,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 3, Application US/08636883
Patent No. 5830691
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IMMEDIATE SOURCE:
CLONE: PUCM010
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E: DNA (genomic)
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Matches 101; Conservative
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; LOCATION: 17..1036
US-08-636-883-3
                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
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ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 175 S. Jefferson Davis Highway, Suite 400 CITY: Arlington STATE: Virginia STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHOD FOR PRODUCING ECTOPROTEIN OF TITLE OF INVENTION: HEPATITIS C VIRUS NUMBER OF SEQUENCES: 9
CORRESPONDENCE, ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,829
57 TTACGTTTGATTTTTCTTTGGGGTTTTGGATTTGTGCT 20
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GENERAL INFORMATION:

APPLICANT: Hendrickson, Eric

APPLICANT: Hendrickson, Eric

TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and

TITLE OF INVENTION: Methods of Regulating DNA Dependent Frotein Kinase Activity

TITLE OF INVENTION: Wethods of Regulating DNA Dependent Frotein Kinase Activity

CURRENT APPLICATION NUMBER: US/09/173,914

CURRENT FILING DATE: 1998-10-16

BARLIER APPLICATION NUMBER: 60/064,557

BARLIER FILING DATE: 1997-10-17

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Kevin P. Anderson et al.
TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C V
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                                                                                                                                                                                             167 acgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttgctgctgt 226
                                                                                                                                                                                                                                                177 TCGGAAGTCTTCCTAGTCGCGCGCACACCCAACCTGGGGCCCCTGCGCGGCAACAGGTAA 118
                                                                                                                                                                                                                                                                                                      227 ggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttcagcagcggggg 286
                                                                                                                                  237 CTACCCTCGGGTTGGCGAGCCTTGGGGATAGGTTGTCGCCTTCCACGAGGTTGCGGCCGC 178
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Best Local Similarity 46.3%; Pred. No. 2.1;
Matches 101; Conservative 0; Mismatches 117; Indels
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                              287 gttctctctttttttttgtggttttgagttggggat 324
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STREET: 66 East Main Street
CITY: Marlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 TTACGTTTGATTTTTCTTTGGGGTTTTGGATTTGTGCT 20
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8.5%; Score 30.4; DE
Best Local Similarity 57.3%; Pred. No. 4.5;
Matches 55; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/08988321B Patent No. 6174868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09173914 Patent No. 6171857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mesocricetus Auratus
US-09-173-914-3
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CORRESPONDENCE ADDRESS:
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LENGTH: 2473
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STATE:
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111 ccacgggcgtccctgctgtcagctctggccgctgccttccagggctcccgagccacacgc 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 gaacctcactttcagaagaagacaaacagtaagcttgggtttttcagcagcggggggttc 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 CACCAACGATCTGACCACCGCCCGGGAACTTGACCTCCTGTGGGCGGCGGTTGGTGTTAC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.4%; Score 30; DB 4; Let 46.3%; Pred. No. 3.1; tive 0; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
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OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.1 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0245
TELECOMMUNICATION INFORMATION:
TELEPHONE: (856) 810-1515
                                                                 US/08/988,321B
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: September 10, 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 25, Application US/08397220B
; Patent No. 6284458
; GENERAL INFORMATION:
                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/650,093
FILING DATE: May 17, 1996
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/397,220
FILING DATE: March 9, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/945,289
                                                                                                                                                                                                                           08/452,841
                                                                                        FILING DATE: December 10, 1997
                                                                                                                                                                                                                                                FILING DATE: May 30, 1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (856) 810-1454
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: Single
                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: NJ
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-397-220B-25/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 gaacctcactttcagaagaagacaaacagtaagcttgggtttttcagcagcgggggttc 290
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Pred. No. 3.1;
0; Mismatches 115; Indels
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Tekahara, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                              OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/01293
FILING DATE: 10-Sep-93
APPLICATION NUMBER: JP S-87195
FILING DATE: 14-Apr-93
APPLICATION NUMBER: 07/945,289
FILING DATE: 10-Sep-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378 GITTGGTTTTCTTTGAGGTTTAGGATTCGTGCT 345
                                                                                                                                                                                                                                                                                                                                                                        NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0031
TELECOMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 tctcattttttttttgtggttttgagttggggat 324
                                                                                                            APPLICATION NUMBER: US/08/397,220B
FILING DATE: 09-Mar-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-397-220B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                  WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08866650 Patent No. 5939321 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: Single
                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.4%;
Best Local Similarity 46.3%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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162 gccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttgct 221
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8.4%; Score 30; DB 2; Length 4771;
Best Local Similarity 52.4%; Pred. No. 8.5;
Matches 66; Conservative 0; Mismatches 60; Indels
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APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                           960296.93839
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APPLICATION NUMBER: US/09/021,287
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South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/866,650
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Patent No. 5981717
                                                                                        FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BETSON, Bennett J
REGISTRATION NUMBER: 37094
REPERNCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                              TELEPHONE: 608-251-5000
TELEPAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEGUENCE CHARACTERISTICS:
LENGTH: 4771 base pairs
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EDNESS: double
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ADDRESSEE: Quarles & STREET: 1 South Pinc.
CITY: Madison
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LOCATION: 611..3652
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COMPUTER:
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8.4%; Score 30; DB 2; Length 4771;
Best Local Similarity 52.4%; Pred. No. 8.5;
Matches 66; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                ;; LOCATION: 611..3652
OTHER INFORMATION: /product= "murine mīll protein"
US-09-031-287.1
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Patent No. 6297011
GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/09/240,473
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-9060
INFORMATION FOR SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 2:
LENGTH: 4771 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
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                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
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APPLICANT: El-Deiry, Wafik
APPLICANT: Uogelstein, Bert
TITLE OF INVENTION: p21WaFl Derivatives and Diagnostic
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                            ; LOCATION: 611..3652
; OTHER INFORMATION: /product= "murine mTll protein"
US-09-240-473-2
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REGISTRATION NUMBER: 32,141
REFERNE/FOCKET NUMBER: 01107.49698
TELECOMMINICATION INFORMATION:
TELEPHONE: 202.508.9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Banner & Allegretti, LTD
STREET: 1001 G Street, NW suite 1100
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                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 7:
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                       LENGIH: 4771 base pairs
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LENGTH: 5143 base pairs
                                                                                                                                                                                                                                                                                                        66; Conservative
SEQUENCE CHARACTERISTICS:
                                 nucleic acid
EDNESS: double
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STRANDEDNESS: double
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                                                                                                                                         NAME/KEY: CDS
LOCATION: 611..3652
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CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                        TYPE: nucleic STRANDEDNESS:
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RESULT 14
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                                                                                                                                                 Query Match

8.4%; Score 30; DB 1; Length 5143;
Best Local Similarity 50.7%; Pred. No. 8.8;
Matches 72; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kinzler, Kenneth W.
APPLICANT: El-Deiry, Wafik
APPLICANT: Vogelstein, Bert
IITLE OF INVENTION: P21WAF1 Derivatives and Diagnostic
IITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.49698
TELECOMMUNICATION INFORMATION:
TELEPRAT. 202.508.9100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Banner & Allegretti, LTD STREET: 1001 G Street, NW Suite 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/574,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08795015 Patent No. 5871968 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               4300 GCCACAAATCTGGCTTTTTTA 4279
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MOLECULE TYPE: DNA (genomic)
                                                     POSITION IN GENOME:
CHROMOSOME/SEGMENT: 6P21.2
US-08-574-043A-7
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ORGANISM: Homo sapiens
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: GM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
EDNESS: double
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08751189
Patent No. 5919656
GENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5919656el Genes Encoding Telomerase Protein TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                             8.4%; Score 30; DB 2; Length 5143; 50.7%; Pred. No. 8.8; tive 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                         4300 GCCACAAATCTGGCTTTTTTA 4279
                                                                                                                                                                                                                                                                                                                                                                                                            255 aacagtaagcttgggtttttca 276
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CLASSIFICATION: 435
ATTONBEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 1:
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CELL LINE: GM
POSITION IN GENOME:
CRROMOSOME/SEGMENT: 6P21.2
US-08-795-015-7
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 48.8'
Matches 81; Conservative
                                                                                                                                        Query Match 8.4%
Best Local Similarity 50.7%
Matches 72; Conservative
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; MOLECULE TYPE: cDNA
US-08-751-189-1
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ZIP: 91320-1789
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GENERAL INFORMATION:

APPLICANT: Harrington, Lea A.

APPLICANT: Robinson, Murray O.

TITLE OF INVENTION: No. 5981707el Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMOREN, Inc.

STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California

ZOUNTRY: USA

ZIP: 91320-1789

MEDIUM TYPE: Floppy disk
COMPUTER: IBMP C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

### APPLICATION NUMBER: US/09/060,836
5166 IGCTIGITIGITCCTCTCCCGATGAIACACTCTTTCTTACTGCCTTCGACGGGCTCCTGGA 5225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5166 TGCTTGTTTCTTCCTCCGATGATACACTCTTTCTTACTGCCTTCGAGGGCTCCTGGA 5225
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48.8%; Pred. No. 11;
tive 0; Mismatches 85; Indels
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Job time: 14180 sec
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PRIOR APPLICATION DATA:
PRIOR APPLICATION UDATA:
APPLICATION UNBER:
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REFERENCE/DOCKET NUMBER: 34,688
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                        US-09-060-836-1
; Sequence 1, Application US/09060836
; Patent No. 5981707
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LENGTH: 7881 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 48.87
Matches 81, Conservative
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; MOLECULE TYPE: CDNA
US-09-060-836-1
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September 20, 2002, 01:23:10 ; Search time 3895 Seconds (without alignments) 1237.076 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                     OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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357
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries EST:\* Database :

em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_vrt:\* em\_esthum:\* em\_estov:\*
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em\_htc:\* em\_estin:\* em\_estmu:\* gb\_est2:\* gb\_htc:\* em\_estba:\* gb\_est1:\* db\_gss:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

244377 HSC12B881 n BG384217 303216 MA ALI92682 TETEAGOON ALO55629 DIOSOPPHII AZ542175 ENTGP86TF AA94462 VZ01168 r AV864011 AV864011 AV862280 AV892280 AU162694 AU165694 AV862022 AV862022 ALIB4552 TETEAGOON BMA49133 TCAAP2 AU135588 AU135588 BB657864 BB657864 Description SUMMARIES BG384217 CNSO2DO1 CNSO0GON AZ542175 AV842237 AV845237 AV864511 AV892280 AUG5654 AUG5654 AUG5659 AUG5659 AUG5659 AUG5659 AUG5694 AUG569 AUG AU135588 BB657864 Z44377 112 112 113 113 113 113 Query Match Length DB Score 71.2 42.4 39.6 37.4 37 36.4 36.4 36.4 Result No. 9 110 113 114 115 115

AL059400 Drosophil BH087817 RPCI-24-3		BG325753 60242464	BB841907 BB841907				BE733920 601569314		AW751638 RC5-CT007				BE748387 601571806	AL069846 Drosophil	AL267021 Tetraodon				4	4	BI886434 ZF637-1-0	AW681359 EST00077	AL057462 Drosophil	AL098787 Drosophil	AL106126 Drosophil	AQ773862 HS_2254_A	
CNSOOCNG BH087817	CNS04PHC	BG325753	BB841907	AQ848626	CNS006ST	BF128237	BE733920	CNS0162E	AW751638	BB843149	BF484412	BE471178	BE748387	CNSOOETV	CNS03Z10	CNS006U0	CNS015P6	CNSOOETV	CNSOOLT2	AU212427	BI886434	AW681359	CNS00BP8	CNS010C9	CNS01604	AQ773862	
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## ALIGNMENTS

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736 bp mRNA linear EST 24-OCT-20 sapiens cDNA clone PLACE1002437 5', mRNA 1127  Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. , Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Su,A., Nakamura,Y., Nagai,T., Sugano,S. and set  tute  co.jp  co.jp  co.jp  co.jp  dedical Science, University of Tokyo, and lines  Homo sapiens"  axon:9606"  CEI00437"  "PLACEI"  "PLACEI"  "PLACEI"  "PLACEI"  "PLACEI"  "PLACEI"  "PLACEI"  "PLACEIT  "PLACEIT	5 otners
bp mRNA clone Craniata; Catarrhini, Y., Ishii, Sikamura, Y., ishii, Sikamura, Y., ishii, Sikamura, Y., ishii, Sience, il Science, il Scien	1/0 C
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AU13588 AU13588 PLACEI Homo sapi. sequence. AU135588.1 GI:10996127 AU135588.1 GI:10996127 Homon sapiens Eukaryota; Metazoa; Chord Mammalia; Eutheria; Prima I, Chases 1 to 736; Ota T., Nishikawa, T., Suz Yamamoto, J., Wakamatsu, A. IRI human cDNA project Unpublished (2000) Genomics Laboratory Helix Research Institute 11532-3 Yama, Kisarazu, Ch Tel: 81-438-52-3951 Fax: 81-438-52-3951 Fex: 81-438-52-3951 Fex: 81-438-52-3951 Full human cDNA project; ONA Virology, Institute; oDNA Virology, Institute; oDNA Virology, Institute of Me Helix Research Institute. Cocation/Colline.PLACEIOO (Ab xref="taxon: Clone."PLACEIOO (All Institute of Me Helix Research Institute. In 736 In	a 199 c
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RESULT 1 AU13588 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE	BASE COUNT ORIGIN

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Similarity
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB657864 RIKEN full-length enriched, 12 days embryo eyeball Mus BB657864 RIKEN for control of the control of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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URL:http://genome.goc.riken.go.jp,
URL:http://genome.goc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-9216
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                              157 cccgagccacacgctggggggtgctggctgagggaacatggcatgttggcctcagctgagg 216
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                                                                                          Gaps
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                                                                                     Indels
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Unpublished (2001)
Contact: Yoshihide Hayashizaki
    DB 9;
Score 144.2; DB 9
Pred. No. 8.3e-28;
                                                                                 0; Mismatches
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40.4%;
                                                                            Matches 181; Conservative
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                                             Best Local Similarity
Query Match
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JOURNAL
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44-00/1994 mRNA linear EST 14-NOV-1994 HSC12B081 normalized infant brain cDNA Homo sapiens cDNA clone c-12b08, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                   Anotes Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 э;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." 185 c 173 g 134 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                   /clone_lib="RIKEN full-length enriched, 12 days embryo
                    Human Genome Sequences. Manm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 CAGTTAATGACCAGCCAC-AGAGTCACAGCTCTGTGCTCTGGCTGCT-CCCTCCAGGGCT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 cccgagccaca-----cgctgggcgtgctggctgagggaacatggcatgttggcct 207
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                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="12 days embryo"
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                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="D230019D04"
                                                                                                                                                                                                                                                                                                                                      /tissue_type="eyeball"
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
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                                                                                                                e mouse tissues.
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="total brain"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
siolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
50 a 87 c 96 g 56 t 3 others
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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1 (bases 1 to 535)
1 (bases 1 to 535)
2 Eakrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                               Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-1zb08
Seq primer: (-21)M13_universal.
Location/Qualifiers
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.7%; Score 73.8; DB 10; Length 292; llarity 94.5%; Pred. No. 3.4e-09; Conservative 0; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             535 bp mRNA linear 303216 MARC 1PIG Sus scrofa CDNA 5', mRNA sequence. BG384217 GI:13308689 EST.
                                                                                                                                                                                                                                                                                                                                                    /clone_lib="normalized infant brain cDNA"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 cccgagccacacgctgggcgtgctggctgag 187
                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-1zb08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 CCCGAGCCACACGCTGGGGGTGCTGGCTGAG 292
                                                                                                                                    Email: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                              Fax: 33160778698
                                                                                                                                                                                                                                                            1. .292
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Best Local Similarity
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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Tetraodon nigroviridis.
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Tetraodon nigroviridis.
Acatinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acatinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acatinopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

I (bases 1 to 982)
I (bases 1 to 982)
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished

2 (bases 1 to 982)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Bernot, A., and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
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                                                                                           /organism="Sus scrofa"
                                                                                                                     /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
Plate: 90 row: G column: 13
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                       /tissue_type="pooled"
/lab_host="DH10B"
                                                 Location/Qualifiers
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Matches 132; Conserv
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/organism="Tetraodon nigroviridis"

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                                           /clone_lib="G" //ote="Genoscope sequence ID : C0AG260CH10SP1-end :
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 910)
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                                                                                                                                                                                             11.9%; Score 42.4; DB 12;
55.0%; Pred. No. 0.86;
Live 8; Mismatches 46;
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/db_xref="taxon:99883"
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                  /clone="260P19"
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Best Local Similarity 55.0°
Matches 66; Conservative
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EM Entamoced histolytica

Eukaryota; Entamocebidae; Entamoceba.

Eukaryota; Entamocebidae; Entamoceba.

El (Abases 1 to 926)

Entermination of clone end sequences from Entamoceba histolytica

HM1:MSS sheared DNA library

L Unpublished (2000)

Contact: Erendan J Loftus

Contact: Erendan J Loftus

Contact: Erendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3343

Email: bjloftus@tigr.org

Clones are derived from the Entamoceba histolytica HM1:IMSS sheared

Contact Inbarary

High quality sequence start: 17 High quality sequence stop: 297. Location/Qualiflers

source

Seq primer: M13-Forward

Class: shotgun

GSS 14-NOV-2000

AZ542175 926 bp DNA linear GSS 14-NOV-200 ENTGP86TF Entamoeba histolytica Sheared DNA Entamoeba histolytica

AZ542175.1 GI:11150635

genomic, DNA sequence. AZ542175

Entamoeba histolytica.

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/urganism="Entamoeba histolytica"
/strain="HM1:IMSS"
/db_zere="texton:5759"
/db_zere="texton:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/rlote="Wector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR). Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Pred. No. 18;
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Best Local Similarity 57.1%;
Matches 68; Conservative
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                                                                                                                                                              AV845237.1 GI:16823451
                                                                                                                                                                                                                                                                                                                                                                      Contact: Nori Satch
Department of Zoology
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Local Similarity 51.5%;
tes 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                           440 bp mRNA linear EST 14-APR-1998 vz0168.r1 Soares_mammary_gland_NDMMG Mus musculus cDNA clone IMAGE:1314471 5', mRNA sequence.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ccctgctgtcagctctggccgctgccttccagggctcccgagccacacgctgggcgtgct 180
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181 ggctgagggaacatggcatgttggcctcagctgaggttgctgctgtggaagaacctc 237
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Contact: Marra MyMouse EST Project
Contact: Marny MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 10.4%; Score 37; DB 9; Length 440; Best Local Similarity 57.3%; Pred. No. 21; Matches 67; Conservative 0; Mismatches 50; Indels
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/clone_lib="Soares_mammary_gland_NbMMG"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 439. Location/Qualifiers
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/dev_stage="4 weeks"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
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I (bases I to 571)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Contact: Nori Satoh
Department of Zoology
  EST 08-NOV-2001
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 533)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="rcieg08c18"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
/tissue_type="whole animal"
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AV845237 Nori Satoh unpublished cDNA library, egg Ciona intestinalis cDNA clone rcieg08c18 3', mRNA sequence.
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Pred. No. 21;
0; Mismatches 80; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: satoh@ascidian.zool.kyoto-u.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Ciona intestinalis"
/db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Kyoto University
Sakyo'ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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98 agttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctc 157
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Matches 75; Conservative
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AV892280 Nori Satch unpublished cDNA library, young adult Ciona intestinalis cDNA clone rclad32b06 3', mRNA sequence.
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1 (bases I to 579)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
                                                                                      1. 571
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="rcieg37m02"
/clone=lib="Nori Satch unpublished cDNA library, egg"
/tissue_type="whole animal"
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Emall: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: satoh@ascidian.zool.kyoto-u.ac.jp.
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="whole animal"
/dev_stage="young adult"
i 116 c 102 g 203 t
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117 c 98 g
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Ciona intestinalis
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322 bp mRNA linear EST 29-APR-1999
AU056364 Oryza sativa mature leaf Nipponbare Oryza sativa CDNA
AU056364
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1to 322)
Yamamoto,K. and Sasaki,T.
Yamamoto,K. and Sasaki,T.
Rice CoNA from mature leaf
Unpublished (1999)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
198 AGAATATGGAGAGCCAAAGATCTGCATGTTCTGTACACTGAACTCTGCTTTTATTGGATC 139
                                                      158 ccgagccacacgctggcgtgctgactgagggaacatggcatgttggcctcagctgaggt 217
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                                                                                                               138 AAAATGCCAACGCTGTGCCAGCAGTAAGAAGAAATATGGAATGCCAGTCAATTGTCAGAA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Gaps

us-09-846-456-2.std.rst

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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetracdon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetracdon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 12-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNSO27E7 872 bp DNA linear GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 242P21 of library G from Tetraodon nigroviridis, genomic survey
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1 (bases 1 to 872)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Weissenbach, J., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Unpublished
           /organism="Ciona intestinalis"
/db_xref="taxon:7719"
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                                                                                                                                                                                                                                                                                                                                                                         216 AGAATATGGAGGCCAAAGATCTGCATGTTCTGTACACTGAACTCTGCTTTCATTGGATC 157
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Best Local Similarity 50.9%; Pred. No. 40;
Matches 84; Conservative 0; Mismatches
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Tetraodon nigroviridis.
Tetraodon nigroviridis
                                                                                                                         /dev_stage="egg"
116 c 99 g
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I (bases 1 to 571) Kohara, Y. and Shin-i,T.

Expressed genes in Ciona intestinalis
Contact: Nori Satoh
Department of Zoology
                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartoidaes; Oryzeae; Oryzea. 1 (bases 1 to 393) Sasaki, T. and Yamamoto, K. Rice cDNA from mature leaf (2000) Unpublished (2000) Contact: Takuji Sasaki
                                                                                                                                                                                                                                                                        Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                             Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT ='RGP'.
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10.1%; Score 36; DB 9; Length 393;
Best Local Similarity 53.6%; Pred. No. 38;
Matches 75; Conservative 0; Mismatches 65; Indels
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Rice mature leaf"
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Fax: 81-298-38-7468
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69 others 179 t 186 g 61 c 377 a BASE COUNT ORIGIN

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Sequence Human DNA

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Copyright (c) 1993 - 2000 Compugen Ltd.
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AX139751 Sequence AX137830 Sequence AX139817 Sequence AX351038 Sequence AX660715 Sequence AX66094 Sequence AX660894 Sequence AX660894 Sequence

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AX060900 AX127764 AX139751 AX127830 AX139817 AX351038

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Sequence Homo sapi Sequence

AX139818 AC021246 AX060713

AX127831

Homo sapi Sequence Sequence

AX127831 AX139818 AC021246 AX060713 AX060892 AX060719 AX060719 AX060908 AX060908 AX127764

AF285167 AX060719

1000.0 221 1000.0 1697 1000.0 1167 1000.0 3231 1000.0 201164 1000.0 2011999 99.3 183999 99.3 183999 99.1 1756 99.1 1756 99.1 1756 99.1 10442 89.1 10442 89.1 10442 89.1 10444 86.0 10474 86.0 10474 86.0 10474 86.0 10474 86.0 10474 87.1 10472 89.1 10474 81.1 10472 81.1 10474 81.1 10474 82.1 10474 83.1 10474 84.1 10474 84.1 10474 84.1 10474 84.1 10474 85.1 10474 86.0 10474 86.0 10474 87.1 10474 87.1 10474 87.1 10474 88

Sequence

Homo sapi Sequence

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AX060894 AF287263 AC103155 AP000302 AP000046

AP000114 AP000190 AC096044 AP001717 AC093942

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U73520 Mus musculu BC016252 Mus muscu

AC015616 Homo sapi

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AC015616 MMMVGR6

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
62 c 73 g 42
                                                                                                  Sequence 4 from Patent W00183746.
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Description

SUMMARIES

Query Match Length DB

Score

Result No. ö

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Mismatches

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Conservative

Matches 221;

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nriosol/ 697 bp mRNA linear PRI 11-MAY-2000
Homo sapiens ATP binding cassette transporter 1 (ABCA1) mRNA,
partial cds.
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/protein_id="AARE9513.1"
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198 c 190 g 156 t 1 others
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University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                   61 ccgggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggc 120
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Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Analysis of hAEC, gene 5' end: additional peptide sequence,
promoter region, and four polymorphisms
Biochem. Biophys. Res. Commun. 271 (2000) In press
2 (bases 1 to 697)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aouizerat, B.E., Fileding, C.J. and Kane, J.P.
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  Length 221;
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  Score 221; DB 6;
Pred. No. 5.4e-49;
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ilarity 100.0%; Pred. No. 5.4
Conservative 0; Mismatches
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1. .697
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1. .>697
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396. .>697
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                       Best Local Similarity
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Length 697;

Score 221; DB 9; Pred. No. 5.7e-49;

100.0%; 100.0%;

Query Match Best Local Similarity

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1167)

Porsch-Ozcurumez,M., Langmann,T., Heimerl,S., Borsukova,H., Kaminski,W.E., Drobnik,W., Honer,C., Schumacher,C. and Schmitz,G. The zinc finger protein 202 (znf202) is a transcriptional repressor of atp binding cassette transporter al (abcal) and abcgl gene expression and a modulator of cellular lipid efflux J. Blol. Chem. 276 (15), 12427-12433 (2001)
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Submitted (05-JAN-2000) Porsch-Oezcueruemez M.K., Institute for
Clinical Chemistry, Universitiy of Regensburg,
FRanz-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY
                                                                  121 getttgeteettgtttttteeeeggttetgtttteteeeetteteeggaaggettgteaa 180
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/function="cholesterol efflux regulatory protein"
/function="cholesterol efflux regulatory protein"
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Homo sapiens partial ABC-1 gene for ATP-binding cassette
transporter-1, 5'UTR and promoter region.
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ABC-1 gene; ATP-binding cassette transporter-1; promoter.
human.
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Porsch-Oezcueruemez, M.K.
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1148. .1167
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/gene="ABC-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-JUN-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
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1 (bases 1 to 1167)
1 (bases 1 to 1167)
2 (bases 2 to 1167)
3 (bases 2 to 1167)
4 Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
5 Analysis of hABCI gene 5' end: additional peptide sequence, promoter region, and four polymorphisms
5 (bases 224 to 1167)
6 (bases 224 to 1167)
6 (bases 224 to 1167)
7 (bases 224 to 1167)
8 (bases 224 to 1167)
                       Gaps
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promoter and exon 1.
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On Jun 23, 2000 this sequence version replaced gi:7769713
Location/Qualifiers
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Willinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aoulzert, B.E., Fielding, C.J. and Kane, J.P.
Direct Submission
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/db_xref="taxon:9606"
/chromosome="9"
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224. .844
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845. .1147
/number=1
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                                                                                                                                                                           PAT 06-FEB-2002
                                                                                                                                                                                                                                                                                                                                                  1 (sites)
Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
Roser-Montus,M.F., Remaley,A. and Santamarina-Fojo,S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 1 08-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Schmitz,G. and Bodzioch,M.
Atp binding cassette transporter 1 (abc1) gene polymorphisms and uses thereof for the diagnosis and treatment of lipid, cardiovascular or inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1047 GCTTTGCTCCTTGTTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAA 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 gtaattgcgagcgaggtgagtgagtgggccgggacccgcagagccgagccgaccttctct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3231;
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                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 221; DB 6; Best Local Similarity 100.0%; Pred. No. 6.3e-49; Matches 221; Conservative 0; Mismatches 0;
                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3 from Patent WO0170810.
AX253452
AX253452.1 GI:16073979
                                                                                                                                                                     3231 bp
Sequence 1 from Patent WOO183746.
AX351029
AX351029.1 GI:18616385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
a 773 c 876 g 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               876 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    809 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                               human.
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of Pieter de Jong. For further details see

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Submitted (11-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

humquery(Sanger.ac.uk Clone requests:

On Jan 15, 2002 this sequence version replaced gi:18121468.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

corresponding to the overlapping clone, as we submit sequences with

corresponding to the overlapping clone, as we submit sequences with

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality)-

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em; EMBL; Sw;

SWISSPROT; Tr:, TREMBL; WP; WORNEPP; Information on the WORMPEP

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Human DNA sequence from clone RP11-217B7 on chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gtaattgogagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCGCAGAGCCGAGCCGACCCTTCTCTC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                            Length 7260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 ggggtaggagaaagagacgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 221; DB 6;
100.0%; Pred. No. 6.6e-49;
ive 0; Mismatches 0;
                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
1765 c 1905 g 1756 t
Patent: WO 0170810-A 3 27-SEP-2001;
Bayer Aktiengesellschaft (DE)
                                                                                Location/Qualifiers
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Matches 221; Conservative
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Direct Submission
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KEYWORDS
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                                                                            FEATURES
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ò g http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping

Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9 RPI1-217B7 is from the library RPCI-11.1 constructed by the group

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sections only once, except for a short overlap sections only once, except for a short overlap.

The true right end of clone RPII-217B7 is at 96717 in this sequence. The true left end of clone RPII-122F10 is at 72980 in this sequence. The true right end of clone RPII-31320 is at 2000 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
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[ (bases 1 to 149034)
Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L., Chong,J.F., Osorlo,J., Remaley,A., Yang,X.P., Haudenschild,C., Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N., Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jure 92411, 92557

/note="Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
27673 a 21138 c 20380 g 27526 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17257 GTAATTGCGAGCGAGCGAGCGGGGCCGGGACCCCAGAGCCGACCCTTCTCTC 17198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly confirmed by restriction digest."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ccgggctgccggcagggcagggcagggagctccgcgcaccaacagagccggttctcagggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                         IMPORTANT: This sequence is not the entire insert of clone RP11-217B7 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                Institutes of Heath, National Heart, Lung and Blood Institute, Bethesda, MD 20892, USA." 84273

//note="Sequence from overlapping clone RP11-122F10
                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Sequence from AF275948 sequenced by National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gtaattgcgagcgagagtgagtggggccgggacccgcagagccgagccttctctc
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HOMO Sapiens ABCAl (ABCAl) gene, complete cds.
AF275948

        Qy
        181
        ggggtaggagaaagaggcgcaaacacaaagtggaaaacag
        221

        Db
        17077
        GGGTAGGAGAAGAGACGCAAACACACAAAAGTGGAAAACAG
        17037

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http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-11.1"
3238. .3278
                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                /clone="RP11-217B7"
                                                                                                                                                                                                                                                                                                                        /chromosome="9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF275948.1 GI:9247085
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                  VECTOR: pBACe3.6
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AF275948
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1. .149034
/organism="Homo sapiens"
/db_xxef="texon:9606"
join[1454. .1674,2581. .25989,40385. .40478,45012. .45153,46423. .46541,67729. .67850,70831. .71007,83960. .84052,89010. .82250,91962. .92101,92433. .92549,96758. .96955,9910. .93907,9428. .98604,100391. .100613,102360. .102581,103642. .103846,104951. .105664,106862. .107033,103642. .108154,109460. .105604,106862. .107033,11385,110646. .110866,112124. .112196,113185,113185,113104. .12196,113187. .112386,113187. .113186,113187. .113101,115297. .115410,116954,11116,115053. .112196,112364,112364,11116,113329,133341. .133485,134526. .134649,133114. .133229,133341. .133485,134526. .134116,13808. .138108. .138114,140469. .14610,140982. .141116,144683.
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/rpt_family="klu"

25038. 25314.

15038. 25314.

15010.25924. 25989,40385. .40478,45012. .45153,46423. .46541,

15010.25924. .25989,40385. .40478,45012. .45153,46423. .46541,

157739. 67850. 70831. .71007.83960. .84052,80010. .89250,

157739. 67850. .951010. .95249,96758. .96955,97702. .97907,

106451. 105064,100862. .107033,108023. .108154,

109460. .109602,109806. .109943,110646. .110866,
Complete genomic sequence of the human ABCA1 gene: analysis of the
                                                                                  2 (bases 1 to 149034)
Santamarina-Fojo, S., Peterson, K. M., Knapper, C. L., Freeman, L. A., Remaley, A. T., Yang, X. - P., Haudenschild, C. C., Blackmon, E. E., Francois, T. L. and Brewer, H. B. Jr.
                                                                                                                                                                                                Submitted (08-JUN-2000) Molecular Disease Branch, National Institutes of Heath, National Heart, Lung and Blood Institute, Bethesda, MD 20892, USA
                        human and mouse ATP-binding cassette A promoter
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jóin(1454. ..1674,25831. .25923)
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1454. ..148034
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2406. .2678
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DAXKQMKKHLKLAKDSSADRFLNSLGREWTGLDTRNNYKVWFNNKGWHAISSFLNVIN
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TFVLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDMYKNOAMADALERFGENRFVS
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LTGDTTVTRGDAFLNXNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGV
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ARLFSDARRLLLYSQKDTSMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYH
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REKLAAABERVLRSNMDILKPILRTLNSTSPFPSKELABATKTLLHSLGTLAQELFSMR
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A Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Collangelo, M., Collins, S., Collymore, A., Cooke, P., Darellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardf, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Morran, E., McGurk, A., Morkenan, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Subramanian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M. (Boyla, Capter for Genome Submission Submission Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker:html
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Center: Whitehead Institute/ MIT Center for Genome Research
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175064)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; M7815; 100% of reads Chemistry: Dye-terminator B49 Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 117571 bases at least Q40 Consensus quality: 145749 bases at least Q30 Consensus quality: 16749 bases at least Q30 Insert size: 185000; agarose-fp Insert size: 17264; sum-of-contigs Quality coverage: 2.9 in Q20 bases; sum-of-contigs Quality coverage: 3.2 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L2510
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                                        Birren, B., Linton, L., Nusbaum, Homo sapiens, clone RP11-1M10
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2735 4415: cont
4716 4515: gap of
5786 5885: gap of
5786 7885: gap of
5886 7879: cont
7880 7979: gap of
7880 9686: cont
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                                                                                     Unpublished 2 (bases 1 to 175064)
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Homo sapiens clone RPll-1M10, WORKING DRAFT SEQUENCE, 39 unordered
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 7.9e-49;
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68438 68537: gap of 100 bp 68538 71458: contig of 2921 bp in length 71459 71559 76888: contig of 5330 bp in length 71559 76888: contig of 5330 bp in length 76889 76989: gap of 100 bp 82114 82213: gap of 100 bp 82214 82213: gap of 100 bp 82214 82213: gap of 100 bp 82214 82213: gap of 100 bp 98220: contig of 6007 bp in length
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                                                                                                                                                                                                                                                                                                          45548: gap of 100 bp

48116: contig of 2568 bp in length

4826: gap of 100 bp

5268: contig of 4402 bp in length

52718: gap of 100 bp

55592: contig of 3874 bp in length
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25707: contig of 3020 bp in length
07; gap of 100 bp
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contig of 2831 bp in length
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Homo sapiens ATP-binding cassette 1 sub-family A member 1 (ABCA1)
and SNAP protein genes, complete cds.
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SOURCE

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NLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP
                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 201144)
Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submitted (13-JUL-2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/number=12

A POCIAL NET WE GEST DEAL PRODUCT AS ELEMBERY THALLOW'S TRUCKEN A VOCIAL INFUTE WERE GEST PRODUCT AS THE GEST PRODUCT AND A VOCIAL INFUENCE OF THE CONTROL O RQVMAEVNKTFQELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMLLDSRDNDHFWE
QQLOGLDWTAQDIVAFLAKHPEDVQSSNGSYYTWREAFNETNQAIRTISRFWECVNLN
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FSWFISSLIPLLVSAGILVVILKLGNLLPYSDPSVVFVFLSVPAVVTILQCFLISTLF SRANLAAACGGIIYFTLYLPYVLCVAMODYVGFTLKIFASLLSPVAFGFGCGGTALFE EQGIGVQWDNLFESPVEEDGFNLTTSVSMMLFNTFLYGVMTWYIEAVFPGQYGIPRPW YFPCTKSYWFGEESDEKSHPGSNQKRISEICMEEEPTHLKLGVSIQNLVKVYRDGMKV PEKEVGKVGEWAIRKLGLVKYGEKTAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTIG WRFORGYTVWRCASVWFGRSVVLTSHSMEECEALCTRMAINWGRFRCLGSVOHLK WRFORGYTIVWRLAGSNPDIKPYODFFGLAFPGSVLEKHRNMLQYQLPSSLSSLARI FSILSOSKKRLHIEDSYSVSQTTLDQVFVNFFANOQSDDHLKDLSLHKNOTVVDYAVLT **GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPAT** SFLQDEKVKESYV" AX092589

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AC021246.2 GI:9119882
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Best Local Similarity 99.5'
Matches 220; Conservative
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148527. .14
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HOMO sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING.
AC021246
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                    PAT 21-MAR-2001
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1 (bases 1 to 69570)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome, clone RP11-1N10
                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183999)
1 (bases 1 to 183999)
2 (compositions and methods for modulating hdl cholesterol and triglyceride levels
Patent: Wo 0115676*A 1 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28910 GCTTTGCTCCTTGTTTTTTCCCCGGTTCTGTTTTCTCCCCCTTCTCCGGAGGCTTGTCAA 28969
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183999 bp
Sequence 1 from Patent W00115676.
AX092889
AX092589.1 GI:13444647
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Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Stoy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tasafaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                     Zimmer, A. and Zody, M.

Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6705871.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                            ..... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                      Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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1834: contig of 863 bp in length

1934: gap of 100 bp

100 bp in length
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14342 15196: contig of 855 bp in length
15197 15296: gap of 100 bp
15297 16123: contig of 827 bp in length
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f 800 bp in length
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f 870 bp in length
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if 851 bp in length
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18041: contig of 869 bp in length
18141: gap of 100 bp
19009: contig of 868 bp in length
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of 844 bp in length
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f 869 bp in length
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10376: contig of 846 bp in length
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13381 14241: contig of 861 bp in length
14242 14341: gap of 100 bp
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contig of 849 bp in length
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12303 12402: gap of
13280: cont
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11423 12302: conf
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16224 17072: cont
17073 17172: gap of
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18142 1900
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JOURNAL
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56 21955; gap of 200 bp 100 bp 100 bp 22832; contig of 867 bp in length 100 bp 23780; contig of 848 bp in length 100 bp 1
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20066: gap of 100 bp
20921: contig of 855 bp in length
21021: gap of 100 bp
21865: contig of 844 bp in length
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30455: contig of 863 bp in length
30555: gap of 100 bp
31410: contig of 855 bp in length
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contig of 861 bp in length
ap of 100 bp
contig of 846 bp in length
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42824: contig of 811 bp in length
42924: gap of 100 bp
43776: contig of 852 bp in length
43876: gap of 100 bp
44752: contig of 876 bp in length
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45724: contig of 872 bp in length
324: gap of 100 bp
46643: contig of 819 bp in length
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28532: contig of 856 bp in length
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29492: contig of 860 bp in length
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                          28: gap of 100 bp 54268: contig of 840 bp in length
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41913: cont
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31410; con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47699: gap of
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/translation="MACWPOCHLLWKNLTFRRQTCQLLLEVAWPLFIFLLISVRL
SYPPEQHECHFPNKAMPSAGTLPWVGGIICNAWNDCFRYFPFGEAGGVGRFNKSIV
ARLESDARFALLYSQKDTSMROMRKVLTALQQIKKSSNLKLQDFLVDNETESGFLYH
NLSLPKSTVDKMLRADVILHKVFLQGYQLHITSLCNGSKSEBHIQLGDOEVSELGLF
KEKLAAAERVLRSNMDILKFILMDVACDDIAHGQLTVPRSAAVAATGDAKPNNMGRET
LLSICAACNPKVEFHERHILEHFSFCVCVSVSLFPARGIVSFSWASFRIWVLWKAVFWQ
HGESMAVWEGQLGGHILEFFSILVG"
363 C 399 9 414 t
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            Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@Hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952) MEDO human CDNA sequencing project supported by Ministry of International Trade and Industry of Japan, CDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, 5'-63'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Centerect), and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ccgggctgcggcagggcagggcgggggctccgcgcaccaacagagccggttctcagggc 120
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oligo capping; fis (full insert sequence).
Homo sapiens Mammary gland cDNA to mRNA, clone_lib:MAMMA1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens cDNA FLJ12192 fis, clone MAMMA1000851.
AK022254
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/dlone="prACE1002437"
/tissue_type="placenta"
/clone_lib="placent"
/note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                      University of Tokyo.
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Best Local Similarity 99.5'
Matches 220; Conservative
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Direct Submission
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TITLE
JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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2 (bases 1 to 1556)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41625 CCGGGCTGCGGCAGGCCAGGGCGGGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGC 41684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 41565 GTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTC 41624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ccgggctgcggcagggcagggcggggggggggggccccccaacagagccggttctcagggc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1
clone:PLACE1002437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                       33 59182: gap of 6 100 bp 100 
                                 30 55329; gap of 100 bp 56197; contig of 868 bp in length 98 56297; gap of 100 bp 57163; contig of 866 bp in length 64 57263; gap of 100 bp 64 58130; contig of 867 bp in length 158230; gap of 100 bp 11 length 158230; gap of 100 length 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40: gap of 100 bp
66684: contig of 844 bp in length
84: gap of 100 bp
                                                                                                                                                                                                                                                                                                                              59082: contig of 852 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
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Pred. No. 1.4e-48;
0; Mismatches 1.
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67751: gap of 100 bp
    contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66685 66784: gap of
66785 6751: cont
67652 6751: gap of
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Isogai, T. and Otsuki, T.
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57164 57263:
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Best Local
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REFERENCE
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NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' = 8'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
                                                                                                                                                        Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
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Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Boyuslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90698)
Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A.
NEDO human CDNA sequencing project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TITGCICCITGITITICCCCGGITCTGTTITCTCCCCTTCTCCGGAAGGCTTGTCAAGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGGCTGCGGCAGGCAGGCGGGGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACU21345 90698 bp DNA linear HTG :
Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING
AC021345
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MAMMA1000851"
/clone=lib="MAMMA1"
/tissue_type="Mammary gland"
/note="cloning vector: pME18SFL3"
a 489 c 586 g 384 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.1%; Score 219; DB 9; L
100.0%; Pred. No. 2.1e-48;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 ggtaggagaaagagacgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location Qualifiers
                                               Unpublished (2000)
2 (bases 1 to 1750)
Isogai,T. and Otsuki,T.
Direct Submission
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Matches 219; Conservative
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                                                                                                      AUTHORS
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Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McBwan, P., McGurk, A., McKenan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pisan, I.C., Pollara, V., Raymond, C., Rilegy, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct Submission
                                                                                                                                                                                                                            Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced g1:6705761.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
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f 863 bp in length
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of 851 bp in length
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f 878 bp in length
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f 914 bp in length
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11832; gap of 100 bp
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23668: gap of 100 bp
24554: contig of 886 bp in length
24654: gap of 100 bp
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55206; contig of 881 bp in length
55306; gap of 100 bp
56165; contig of 859 bp in length
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97.2%; Score 214.8; DB 2;
Best Local Similarity 99.1%; Pred. No. 3.5e-47;
Matches 216; Conservative 0; Mismatches 2;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human ATP binding	Human ATP binding	Human ABC1 genomic	Human cDNA clone (	Human cDNA sequenc	Human cDNA clone (	Human cDNA sequenc	Human polynucleoti	Human ABCA1 homolo
ΩI	AAD21326	AAI70315	AAF92831	AAH07432	AAH18606	AAH04729	AAH17451	AAK51683	ABA09200
99	22	22	22	22	22	22	22	22	22
% Query Match Length DB	7260	7260	183999	736	1556	763	1750	7281	7086
% Query Match	100.0	100.0	8.66	99.3	99.3	99.1	99.1	93.2	92.9
Score	221	221	220.6	219.4	219.4	219	219	206	205.4
Result No.	Т	7	3	4	2	9	7	80	თ

(FARB ) BAYER AG

G (4)	Nuclectide sequenc Partial human ABC1 Human ABC1 DNA seq Nuclectide sequenc Nuclectide sequenc Human cancer agent	Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc	NUCLEOLUE SEQUENC HSV-2 Strain SB5 C Human herpesvirus Human nervessvirus Human aggrecan deg Human aggrecan deg Human oRFX ORF990 Human i MEXA ORF990	
AAK52667 AAS06121 AAC09615 AAF24680 AAF24702 AAF24686 AAF24686	AAF24708 AAS04035 AAS06120 AAF24681 AAF24703 AAS60816	AAF24680 AAF24702 AAF24685 AAF24707	AAF 24 / UB AAV 62176 AAD 25519 AAD 25519 AAX 00726 AAX 00726	AAK82979 AAS83553 AAS81688 AAK81810 AAK84386 AAX53491 AAX53491 AAX73455
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992.9 892.9 899.1 899.1 86.0 86.0	5.1.1.1.0	15.5 15.5 15.5 15.5		114.6 114.6 114.6 114.6 114.6 114.6
205.4 205.197 197 197 190 190	190 92 91 91 34.4			10000000
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## ALIGNMENTS

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Human, ATP binding cassette transporter 1; ABC1; coronary heart disease; dermatological, atherosclerosis; cardiovascular; inflammatory disease, psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
                                                                                              Human ATP binding cassette transporter 1 (ABC1) gene.
                                                                                                                                                                                                                                              /product= "Human ABC1 protein"
                                                                                                                                                                                                          Location/Qualifiers 321..7106
                      AAD21326 standard; DNA; 7260 BP.
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                                                                       28-JAN-2002 (first entry)
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                                                                                                                                                                                    Homo sapiens
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                                              AAD21326;
          AAD21326
RESULT
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variation

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                                                                                                                                                                                     The invention relates to four common polymorphisms in the gene encoding ATP-binding cassette transporter-1 (ABC1). ABC1 is associated with decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in ABC1 directly affects cellular lipid homeostasis, which is a key factor in the atherogenetic processes. The ABC1 polymorphisms are useful for diagnosing and treating lipid disorders, cardiovascular diseases (coronary heart diseases, atherosclerosis) and inflammatory diseases (psoriasis, lupus erythematosus). The identification of ABC1 as a transporter for interleukin-lbeta (IL-lbeta) identifies this gene as a candidate for treatment of inflammatory diseases including rheumatoid
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501.7106
/*tag= b
/note= "alternative open reading frame of AAI70314"
                                                                                  New adenosine triphosphate binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cholesterol; cardiovascular disease; inflammatory disease; antiinflammatory; antilipaemic; antipsoriatic; dermatological; Tangler disease; coronary heart disease; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP binding cassette transporter 1; ABC1; human; lipid disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 7260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 221; DB 22;
100.0%; Pred. No. 8.7e-55;
iive 0; Mismatches 0;
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                                                                                                                                                        Example 1; Fig 1; 48pp; English.
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Bodzioch M;
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Schmitz G,
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The present sequence is that of cDNA encoding the human adenosine triphosphate (ATP) binding cassette transporter 1 (ABC1) protein (see AAM50227). The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AAT70314, using an alternative ATG codon as initiation codon and thereby adding an extra 40 N-terminal amino acids to the encoded ABC1 protein (see AAM50228). The invention provides 4 common polymorphisms in the ABC1 gene. These were identified by sequencing the ABC1 gene in Card ferent Tangier kindreds. In the variant genes (numbering as in AAT0314), G is changed to A at position 596, T is changed to C at position 1136, A is changed to G at position 589 or G is changed to C at position 136, A is changed to G at position 3456, or any combination of these polymorphisms alter the amino acid sequence of ABC1 and therefore may affect its function. The 2 most common polymorphisms (G596A) and A2589G) are both associated with a decreased in vitro ApoA-I mediated efflux of cholesterol from monounclear phagocytes, a feature typical of Tangier disease. 3 of the variants (G596A) are significantly increased in a population of eature typical of Tangier disease. (CHD) relative to CHD-free control subjects. The use of the provided ABC1 polymorphisms for the diagnosis and treatment of lipid disorders, cardiovascular diseases, and inflammatory disease (CHD) relative to CHD-free control subjects. The use of the provided ABC1 transcribts or diseases, and inflammatory disease (CHD) relative to CHD-free cortol subjects is claimed. Modulation of ABC1 transcribts or proteins by antisense or ribozyme technology or RNA decoys is also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           New adenosine triphosphate binding cassette transporter gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
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replace(3836,C)
eplace(1516,C)
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                                                                                                                                                                                                                                                                                                                                                       Schmitz G, Bodzioch
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(HDL-C) level, a higher than normal trigilyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity
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                                   181 ggggtaggagaagagacgcaaacacaaaagtggaaaacag
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                                                                                                                                                                                                                                      AAF92831 standard; DNA; 183999
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2000US-0213958
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ABC1 genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-244356/25
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15-MAR-2000;
23-JUN-2000;
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                                                                        28910 gctttgctccttgtttttccccggttctgttttcccccttctccggaaggcttgtcaa 28969
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                                                                                                                                                     ccgggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggc 120
                                                                                                                                                                                                                             getttgeteettgttttteeeeggttetgtttteteeeetteteeggaaggettgteaa 180
                                        Gaps
Score 220.6; DB 22; Length 183999;
Pred. No. 3.1e-54;
1; Mismatches 0; Indels 0; G
                                                                                                                                                                       1; Mismatches
   99.8%;
99.5%;
                                        Conservative
                     Best Local Similarity
                                        220;
 Query Match
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Matches

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The present invention describes primer sets for synthesising 5602

[ull-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligounclectide complementary
to the complementary strand of a polynuclectide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises at 3'-end sequence. Where the
complementary strand of a polynucleotide which comprises a 6'-end
sequence and an oligonucleotide comprises at 3'-end sequence.
CC complementary to the
complementary strand of a polynucleotide which comprises at least 15 nucleotides and the combination of
the 5'-end sequence 3'-end sequence is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
connected and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH03628 and
AAH13633 represent human amino acid sequences; and AAH13629 to AAH13632
cepresent cligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                             Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito K,
                     28970 ggggtaggagaaagagacgcamacacaaaagtggaaaacag 29010
181 ggggtaggagaaagagacgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID 4267; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagai K,
                                                                                                                                                                                                                                                                      Human cDNA clone (5'-primer) SEQ ID NO:4267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashi K,
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                          AAH07432 standard; cDNA; 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                              (first entry)
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09-JUN-2000;
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                                                                                                                         AAH07432
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Sequence 736 BP; 163 A; 199 C; 199 G; 170 T; 5 other;

Query Match

99.3%; Score 219.4; DB 22; Length 736;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonuclectide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
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                                                                          gtaattgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctc
                                                                                                                            1 gtagttgcgagcgagagtgagtggggccggggacccgcagagccgagccttctctc
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  No. 1.3e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai T, Nishikawa T, Hayashi K, Sa
Sugiyama T, Wakamatsu A, Nagai K,
                         0; Mismatches
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     Pred.
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
99.58;
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                            220; Conservative
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  Best Local Similarity
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Ishii S,
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                         Matches
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AAH18606
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in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13639 to AAH13629 and AAH13639 represent human cDNA sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                        121 getttgetecttgtttttteeeeggttetgtttteteeeetteteeggaaggettgteaa 180
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                                                                                                                                                                                                     Score 219.4; DB 22; Length 1556; Pred. No. 1.6e-54;
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                                                                                                                                                                                                                                     1; Indels
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Otsuki T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA clone (5'-primer) SEQ ID NO:1564.
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                                                                                                                                                                                                                                     Mismatches
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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                                                                                                                                of the present invention.
                                                                                                                                                                                                                                     Matches 220; Conservative
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                                                                                                                                                                                                         Query Match
Best Local Similarity
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the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNas. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNas. The primers allow obtaining of the full-length cDNas asaily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                     complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                       oligonucleotide comprises at least 15 nucleotides and the combination of
                   The present invention describes primer sets for synthesising 5602 full-inedth coNns defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
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Sequence 763 BP; 137 A; 205 C; 260 G; 158 T; 3 other;

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                                                                                                                                                              121 tttgeteettgtttttteeeeggttetgtttteteeetteteeeggaaggettgteaagg 180
                        Gaps
                                             3 aattgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctccc 62
                                                                   1 aattgcgagcgaggtgagtggggccgggacccgcagagccgagccgaccttctctccc 60
                      0;
99.1%; Score 219; DB 22; Length 763; 100.0%; Pred. No. 1.7e-54;
                      Indels
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       100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                      Human cDNA sequence SEQ ID NO:16905
                                                                                                                                                                                                                                                                   AAH17451 standard; cDNA; 1750
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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          Best Local Similarity 100.0
Matches 219; Conservative
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11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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polynuclectide which comprises a 3'-end sequence, where the comprises at least 15 nuclectides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynuclectides, particularly full-length convex. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs as also useful for the AAH13633 to AAH13632 and AAH13633 to AAH13632 to AAH13632 represent human anino acid sequences; and AAH13639 to AAH13632 represent oligonuclectides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                          The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggcgc 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 gggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggcgc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 tttgctccttgttttttccccggttctgttttcccccttctccggaaggcttgtcaagg 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 tttgeteettgtttttteeeeggttetgtttteteeeetteteeggaaggettgteaagg 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 aattgcgagcgagagtgagtggggccgggacccgcagagccgagccttctctcccc 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 aattgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctccc 60
                                                               Yamamoto J;
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                                                            Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1750 BP; 291 A; 489 C; 586 G; 384 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.1%; Score 219; DB 22;
100.0%; Pred. No. 2.2e-54;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 ggtaggagaaagagacgcaaacacaaaagtggaaaacag 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 ggtaggagaaagagacgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID 16905; 2537pp + CD ROM; English.
                                                                                  Nagai K,
                                                               Hayashi K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK51683 standard; cDNA; 7281 BP
                                                               Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2001 (first entry)
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Best Local Similarity 100.
Matches 219; Conservative
                (HELI-) HELIX RES INST.
                                                                                      Sugiyama T,
                                                                                                                                 WPI; 2001-318749/34.
                                                            Isogai T,
                                                                                                                                                                                                                                            full-length cDNAs
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                                                                                    Ishii S,
                                                               Ota T,
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or eptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                               Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment of cancer, leukaemia, nervous system disorders, arthritis and
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vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                         Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                       Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y. Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1086-1096; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in diagnosis and gene therapy
                                                                                                                                                                                                                              2000us-0560875.
2000us-0508075.
2000us-0620125.
2000us-063861.
2000us-0663561.
                                                                                                                                                                           05-FEB-2001; 2001WO-US04098.
                                                                                                                                                                                                                                                                              01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0663561.
20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                               2000US-0496914
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                                                                                                        WO200157190-A2.
                                                                                                                                                                                                                               27-APR-2000;
20-JUN-2000;
19-JUL-2000;
                                                                          Homo sapiens.
                                                                                                                                                                                                             03-FEB-2000;
                                                                                                                                           09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                96 gcggcagggcagggcgggggggggctccgcggcaccaacagagccggttctcagggcgctttgc 155
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                        36 cgatttcgtgtgagtggggccgggacccgcagagccgagccgaccttctctcccgggct 95
                                                                                                                                                                                                                                                                                                                             8 cgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctcccgggct 67
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0
                                                                                                                                                                                                                                                                                                    93.2%; Score 206; DB 22; Length 7281; 97.7%; Pred. No. 2.1e-50;
                                                                                                                                                                                                                                                                                  Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                      gagaaagagacgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                                                                                                                                                  216 gagaaagagacgcaaacacaaaagtggaaaacag 249
                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                           Best Local Similarity 97.73
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                     Query Match
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; haematopoiesis chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; oronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                    Human ABCAl homologue-encoding cDNA, SEQ ID NO:976.
                                                                             ABA09200 standard; cDNA; 7086 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2001; 2001WO-US03800.
                                                                                                                                                                                                                                                     11-JAN-2002 (first entry)
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                                                                                                                                                                       ABA09200;
                                    ABA09200
RESULT
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Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammallan subject e.g. arthritis and cancer 2001-457740/49. P-PSDB; ABB11956.

Tang YT, Liu C, Drmanac RT;

(HYSE-) HYSEQ INC.

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

Claim 1; Page 833-835; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The convention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, and methods of identifying compounds which bind to polypeptides of the invention have homology to known proteins, thereby compounds of the invention have homology to known proteins, thereby polypeptides of the invention have homology to known proteins, thereby compared in instably into their probable bollogical activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell effect activity; activity; tissue growth activity; hammonodulatory activity; tissue growth activity; hammonodulatory activity; activin or inhibin-related activities; communicatic or chemotratics activities; hammonodulatory activity; activin or inhibin-related activities; communication activities; activities; hammonodulatory activities; activities, hammonodulatory activities; activities, polypeptides and nucleotides of thrombolytic activities; activities, polypeptides and nucleotides of thrombolytic activities; activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include cancers, hammatopoletic disorders (e.g., mypeloid or lymphoid cell activities) and abnormal arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

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vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 ggcagggcggggggggctccgcgcgcaccaacagagccggttctcagggcgctttgctccttgt 124
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                   gagtgagtggggccgggacccgcagagccgagccgaccttctctccccgggctgcgggag
                                                                                                                                                                                                                                                                                  22; Length 7086;
                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                  Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
                                                                                                                                                                                                                                                                                  Score 205.4; DB 22; Length
Pred. No. 3.2e-50;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 agacgcaaacacaaaagtggaaaacag 221
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2000US-0598075.
2000US-0620325.
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2000US-0693325.
2000US-0728422.
                                                                                                                                                                                                                                                                                  Match 92.9%;
Local Similarity 99.5%;
Les 206; Conservative
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15-SEP-2000;
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Best Local Si
Matches 206;
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Ma Y;

Cao Y,

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Liu C, Drmanac RT, Asundi V, Zhou P,

Tang YT,

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that exhibit activity elating to
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                                                                                                                                                                                                                                                                                                                                                          (AAM80020) are omitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 gagigaagiggggccgggacccgagagccgagccgaccttctctcccggggctgcggcag 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 205.4; DB 22; Length 7086; pred. No. 3.2e-50; 0; Mismatches 1; Indels 0;
 Wang
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
Wang D, Wang J, Zhang J, Ren F, Chen R,
Yang Y, Wejhrman T, Goodrich R;
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/product= "Human ABC1 protein"
                                                                                                                                         Claim 1; Page 4558-4560; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                          were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221
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298..7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 agacgcaaacacaaaagtggaaaacag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS06121 standard; cDNA; 9854
                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.9%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ABC1 DNA sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                             WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                               P-PSDB; AAM79534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200130848-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                 inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS06121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
    Shao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
                   Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS06121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                            The sequence represents the coding sequence #2 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological pathologies, and other diseases e.g. Tangler disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                    Naudin L;
                                                                                                                              Brewer HB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cagggcgggggggctccgcgcaccaacagagccggttctcaggggcgctttgctccttgttt 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 gtgagtggggccgggacccgcagagccgagccgaccttctccccggggctgcggcaggg 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                              Rosier-Montus M, Arnould-Reguigne I, Prades C,
Duverger N, Jaye M, Searfoss GH, Remaley A, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9854;
                                                                                                                                                                                                  New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.8%; Score 205; DB 22;
100.0%; Pred. No. 4.6e-50;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein 5' EST, SEQ ID NO: 13690.
                                                                                                                                                                                                                                        Claim 1; Page 209-213; 368pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-OCT-2000; 2000WO-EP10886.
                                                            01-MAR-2000; 2000US-0186260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC09615 standard; cDNA; 227
                                                  99EP-0402668
                                                                                     (AVET ) AVENTIS PHARMA SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0
Matches 205; Conservative
                                                                                                                                                             WPI; 2001-316327/33.
                                                                                                                                                                            P-PSDB; AAU02176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5' EST;
                                                26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
 03-MAY-2001
                                                                                                              Denefle P,
Lemoine C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC09615;
                                                                                                                                         Dean M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human;
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 ccgggctgcggcagggcagggcggggggggctccgcgcccaacagagccggttctcagggc 150
                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ccgggctgcggcagggcagggcggggggggggccccaacagagccggttctcagggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 getttgeteettgtttttteeeeggttetgtttteteeeetteteeggaaggettgteaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 227 BP; 44 A; 65 C; 73 G; 45 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 197; DB 21;
Pred. No. 3.1e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of a human ABC1 polypeptide.
                                                                                                                                                                                                            Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID 13690; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.1%; Scor.
100.0%; Pred. No. 5.-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression and secretion vectors.
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                                                 21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 ggggtaggagaaagaga 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ggggtaggagaagaga 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                         Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                             WPI; 2000-500381/45.
                                                                                                                                                        (GEST ) GENSET
                                                                                                    26-FEB-1999;
06-SEP-2000
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us-09-846-456-4.std.rng

(first entry)

20-APR-2001

AAF24702;

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The present sequence encodes a human adenosine triphosphate (APP)
binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
membranes and utilises ATP hydrolysis to transport a wide variety of
membranes and utilises ATP hydrolysis to transport a wide variety of
ubstrates across the plasma membrane. ABC1 is a pivotal protein in
the apolipoprotein-mediated mobilisation of intracellular cholesterol
stores. ABC1 is defective in Tangier disease, a genetic disorder
characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
localised to chromosome 9422-9431. The ABC1 genes and proteins are
useful for developing pharmaceutical agents for the treatment of heart
disease and other disorders associated with hypercholesterolemia and
atherosclerosis. The genes are useful for developing screening assays to
screen for compounds that regulate the expression of genes associated
with cholesterol transport. The genes and proteins are also useful for
the disorders associated with hypercholesterolemia.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gttetgtttteteeeetteteeggaaggettgteaaggggtaggagaaagagaegeaaae 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.1%; Score 197; DB 22; Length 10442; 100.0%; Pred. No. 1e-47; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;
                                                                                                                                     /product= "ABC1 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 122-128; 215pp; English.
                                             Location/Qualifiers
291..7076
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                          99US-0140264.
99US-0153872.
99US-0166573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wade D, Garvin M;
                                                                                                                                                                                                                                                                                                                   2000WO-US16765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CVTH-) CV THERAPEUTICS INC.
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Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-137812/14.
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                                                                                                                                                                                               WO200078972-A2
                                                                                                                                                                                                                                                                                                                   16-JUN-2000;
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                             18-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25
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AAF24702 standard; DNA; 10442 BP.

RESULT 14

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AAF24702 ID AAF2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggagetccgcgcaccaacagagccggttctcagggcgctttgctccttgtttttccccg 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                             Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other disorders associated with hypercholesterolemia
                                                                                   Nucleotide sequence of a human ABC1 polypeptide.
                                                                                                                                                                                                                                                                                                   /product= "ABC1 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garvin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 117-123; 211pp; English
                                                                                                                                                                                                                                            Location/Qualifiers
291..7076
                                                                                                                                                                                                                                                                                                                                                                                                             16-JUN-2000; 2000WO-US16591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oram JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0166573
                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0140264
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawn RM, Wade D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAB31365
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61 ggagctccgcgcaccaacagagccggttctcagggcgctttgctccttgtttttccccg 120
                    205 acaaaagtggaaaacag 221
                                                                                181 acaaaagtggaaaacag 197
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Nucleotide sequence of ABC1 polypeptide from Tangier disease patient. AAF24685 standard; DNA; 10474 BP 20-APR-2001 (first entry) AAF24685; 

Human; adenosine triphosphate binding cassette protein 1; ABC1; applipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9q22-9q31; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.

Homo sapiens

/\*tag= a /product= "defective ABC1 polypeptide" Location/Qualifiers 323..7108

WO200078972-A2

28-DEC-2000

99US-0153872. 99US-0140264 18-JUN-1999; 19-NOV-1999;

16-JUN-2000; 2000WO-US16765.

(CVTH-) CV THERAPEUTICS INC.

Wade D, Garvin M; Lawn RM,

WPI; 2001-137812/14.

Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis

Disclosure; Page 148-154; 215pp; English.

The present sequence encodes a human adenosine triphosphate (ATP)

binding cassette protein (ABC) 1 polypeptide, and is isolated from
a Tandier disease patient. ABC1 resides in cell membranes and utilises
ATP hydrolysis to transport a wide variety of substrates across the
plasma membrane. ABC1 is a pivoteal protein in the apolipoprotein-mediated
mobilisation of intracellular cholesterol stores. ABC1 is defective in
Tangier disease, a genetic disorder characterised by abnormal
HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
9422-9431. The ABC1 genes and proteins are useful for developing
pharmaceutical agents for the treatment of heart disease and other
disorders associated with hypercholesterolemia and atherosclerosis. The
genes are useful for developing screening assays to screen for compounds
transport. The genes and proteins are also useful for are also useful
as diagnostic indicators of cardiovascular disease and other disorders
associated with hypercholesterolemia.

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136 tittccccggttctgttttctccccttctccggaaggcttgtcaaggggtaggaaaga 195
                                                                                                                                                                                                                       Gaps
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                                                                                                                     24 agcaagetteggeacgageegragageegageegaeeetteteteeegggetgeggeagg 83
                                                                                             16 agtgagtggggccgggacccgcagagccgagccttctctcccccgggctgcggcagg
                                                                 ;
0
                                         Length 10474;
Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;
                                                                   10; Indels
                                      Score 190; DB 22;
Pred. No. 1.1e-45;
0; Mismatches 10;
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                                     vuery Match 86.0%;
Best Local Similarity 95.1%;
Matches 196; Conservative
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Search completed: September 20, 2002, 03:09:16 Job time: 10625 sec

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September 20, 2002, 03:21:31; Search time 110.16 Seconds (without alignments) 492.783 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                 383533 seqs, 122816752 residues
                                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                       US-09-846-456-4
221
                                                                                                                                                                                                   Title:
Perfect score:
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                                                                                                                      Run on:
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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2: /cgn2\_6/ptcdata/2/lna/5B\_COMB.seg:\*
3: /cgn2\_6/ptcdata/2/lna/6A\_COMB.seg:\*
4: /cgn2\_6/ptcdata/2/lna/6B\_COMB.seg:\*
5: /cgn2\_6/ptcdata/2/lna/PCTUS\_COMB.seg:\*
6: /cgn2\_6/ptcdata/2/lna/PCTUS\_COMB.seg:\* Issued\_Patents\_NA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 7, Appli	7,	4,	4	8	4	4	θ,	ω,	m	ω,	Ä	H	1	٦,	1,	H	2,	5	1,	1,	m	'n	H	<u>-</u>	a)	Sequence 1, Appli
SUMMARIES	US-09-191-171-7	US-09-385-707-7	-08-327	-08	US-08-713-928B-8	US-09-191-171-4	US-09-385-707-4	US-08-871-572B-3		US-08-745-880-3	US-08-480-382-3	US-09-335-409-1	US-09-568-102-1	US-09-567-969-1	US-09-568-480-1	US-09-568-486-1	US-09-568-472-1	US-09-443-501A-2	US-09-167-354-5	US-08-455-001-1	PCT-US95-11869-1	US-08-793-035-3	US-09-429-322-3	US-08-125-468-1	US-08-474-933-1	US-09-103-840A-2	US-09-103-840A-1
Length DB	4480 3	4480 4	3509 2	3509 2	2067 2	2155 3	2155 4	2255 4	4405 1	4405 2	4405 2	68750 3	68750 4	68750 4	68750 4	68750 4	68750 4	71989 4	2699 3	1809 1	1809 5	1299 3	2754 4	30001 1	30001 2	4403765 4	111529 4
% Query Match Le	13.9	13.9	13.8	13.8	13.8	13.8	•	13.4	13.4	13.4	13.4	4.	13.4 (	3.4	4.	13.4	4.	4.	13.3	13.2	13.2	13.1	13.1	0.	0	0.	13.0 44
Score	30.8	30.8	30.6	30.6	30.4	30.4	30.4	29.6	29.6	29.6	29.6	29.6	σ.	29.6	σ	9	29.6	S.	29.4	29.2	29.5	29	7	28.8	28.8	28.8	28.8
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US-08-755-559-2 US-09-210-474-2 US-09-539-774-2 US-08-943-731-5 US-08-78-7340-1 US-08-78-7340-1 US-08-439-009A-1 US-08-570-311-5 US-08-570-311-5 US-08-570-311-5 US-08-570-311-5 US-08-570-311-5 US-08-353-485-5 US-08-353-484-42 US-08-353-48-5 US-08-455-556-42
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SCOTT, Hamish S.
APPLICANT: ANSON, Donald S.
APPLICANT: ANSON, Annette M.
APPLICANT: ORSBORN, Annette M.
APPLICANT: CLEMENTS, Peter R.
APPLICANT: MORRIS, Charles P.
APPLICANT: MORNIS, Charles P.
APPLICANT: MORNOD, John J.
TITLE OF INVENTION: SYMTHETIC ALPHA-L-IDURONIDASE AND GENETIC
TITLE OF INVENTION: SEQUENCES ENCODING SAME
                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                            Query Match 13.9%; Score 30.8; DB 3; Length 4480; Best Local Similarity 53.3%; Pred. No. 6.4; Matches 65; Conservative 0; Mismatches 57; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/385,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/494,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89782
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REGISTRATION NUMBER: 31,346
REPERENCE/DOCKET NUMBER: 89782
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELERX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09385707
Patent No. 6238662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 4480 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                             TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-191-171-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: SCOTT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
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ZIP: 11530
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APPLICANT: Strong Santa J.

APPLICANT: Strong Santa J.

APPLICANT: Strong Santa J.

APPLICANT: Strong Santa J.

TITLE OF INVENTION: Transcription Factor Regulating MHC

TITLE OF INVENTION: Expression, cDNA and Genomic Clones Encoding Same and

TITLE OF INVENTION: Retroviral Expression Contructs Thereof

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner, Birch, McKie & Beckett

STREET: 1001 G Street, N.W.
                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                            2715 CIGCGGTIGGGGTGGGGGGGTGTCGTCGCTCGCGTAGATCAGCACCGCGGGGGGCGCCAG 2656
                                                                                                                                                                                                                                                                                                                                                        66 ctgcggcagggcagggcggggggggctccgcgccaacagagccggttctcagggcgctt 125
                                                                                                                                                                                                                                                           6 tgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctcccggg 65
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                                                                                                                                                         Query Match 13.9%; Score 30.8; DB 4; Length 4480; Best Local Similarity 53.3%; Pred. No. 6.4; Matches 65; Conservative 0; Mismatches 57; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: POSOTSKé, Laurence H.
REGISTRATION NUMBER: 34.698
REFERENCE/DOCKET NUMBER: 1107.46362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 20-2 508-9153
TELEPAX: 202 508-929
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08327832
Patent No. 5840832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington, D.C. STATE: District of Columbia
                                                    , MOLECULE TYPE: DNA (genomic) US-09-385-707-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 3509 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
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MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
TYPE: nucleic acid
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                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-327-832-4/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION:
US-08-327-832-4
                                             TOPOLOGY:
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                                                                                                                                                                   Query Match
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70 ggcagggcagggcggggggggctccgcgcaccaacagagccggttctcagggcgctttgctc 129

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GENERAL INFORMATION:
APPLICANT: Onc. Santa J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: Transcription Factor Regulating MHC
TITLE OF INVENTION: Expression, cDNA and Genomic Clones Encoding Same and
TITLE OF INVENTION: Retroviral Expression Contructs Thereof
NUMBER OF SEQUENCES: 16
                                                  ö
                                                                                                                                                                                                                    2521 TGCAGGGCTGCTTGCAGGCTCACAAGACACTCCCTTTGTGACAGAGTCTCTGAC 2462
                                                                                                                                         2581 AGGGTGAGCTGGTATGGCAGGGTGCCATACAGGGGTGCCCACAGTCAGCTCTGGGGGTGG 2522
                                                                                                                                                                                       0; Gaps
                                                                                              10 agcgagagtgagtgggggccgggacccgcagagccgagccgaccttctctcccgggctgc 69
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Score 30.6; DB 2; Length 3509;
Pred. No. 6.7;
0; Mismatches 64; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1107.46362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: POSOTSKe, Laurence H.
REGIESTRATION NUMBER: 34,698
REFRENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 20-2 508-9153
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3509 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-08-828-584-4/c
; Sequence 4, Application US/08828584
; Patent No. 5908762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
  Query Match 13.8%;
Best Local Similarity 51.9%;
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3509 base pai
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                 2461 ATTTGTGCATCCC 2449
                                                                                                                                                                                                                                                                                   130 cttgttttttccc 142
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.3312
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2521 TGCAGGGCTGCTTGCAGGGCTCATCCACAAGACACTCCCCTTTGTGACAGAGTCTCTGAC 2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: RADIN, DAVID N.
APPLICANT: CRAMER, CAROLE L.
APPLICANT: OTSHI, KAREN K.
APPLICANT: WELSENBORN, DEBORAH L.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PRANT-BASED EXPRESSION SYSTEMS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1340 cGGGTGTCGTCGCTCGCGTAGATCAGCACCGCGGGGGCGCCAGGC 1297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30.4; DE Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 7956-0011-999
TELECOMMUNICATION IRPORMATION:
TELEFHONE: (212) 790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,928B
FILLIG DATE: 13-SEP-1996
CLASSIFCATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/003,737
FILING DATE: 14-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                        Sequence 8, Application US/08713928B Patent No. 5929304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
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ilarity 55.8%;
Conservative
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                                                                                          2461 ATTTGTGCATCCC 2449
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                                                   130 cttgttttttccc 142
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Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                   US-08-713-928B-8/c
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RESULT

2581 AGGGTGAGCTGGTATGGCAGGGTGCCATACAGGGGTGCCCACAGTCAGCTCTGGGGGTGG 2522

Best Local Similarity 51.99
Matches 69; Conservative

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1428 CGGGTGTCGTCGCTCGCGTAGATCAGCACCGCGCGCGCCCAGGC 1385
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; LOCATION:
US-09-385-707-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-08-871-572B-3
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                                                                                                                                                                         APPLICANT: SCOTT, Hamish S.
APPLICANT: ANGON, Donald S.
APPLICANT: ANGON, Donald S.
APPLICANT: ORSBORN, Annette M.
APPLICANT: ORSBORN, Annette M.
APPLICANT: CLEMENTS, Deter R.
APPLICANT: HORWIS, Charles P.
APPLICANT: HORWOOD, John J.
TITLE OF INVENTION: STOUTHERIC ALPHA-L-IDURONIDASE AND GENETIC TITLE OF INVENTION: SEQUENCES ENCODING SAME
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,171
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FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/494,104
FILING DATE: 14-NOV-1991
FILING DATE: 14-NOV-1991
FILING DATE: 14-NOV-1991
PRIOR APPLICATION DATA:
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,254
FILING DATE: 07-NOV-1992
APPLICATION NUMBER: US 08/084,254
FILING DATE: 07-UUL-1993
APPLICATION NUMBER: 1993
APPLICATION NUMBER: 1998
AFTORNEY AGENT INFORMATION:
NAME: DiGIGILO, FTANK S.
REGESTRANTON NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 89782
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION
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                                   Sequence 4, Application US/09191171
Patent No. 6149909
Patent No. 6149909 6143294
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MEDIUM TYPE: Floppy disk
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Matches 58; Conservative
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; LOCATION: 89..2047
US-09-191-171-4
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                                                                                                                                             GENERAL INFORMATION:
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ZIP: 11530
US-09-191-171-4/C
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1488 GGGCGGGGGGGACCCCGCGCAGCCACGCTCACCGCGACGCTGCGGTTGGGGTGGGCG 1429
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                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: SCOTT, Hamish S.
APPLICANT: SCOTT, Hamish S.
APPLICANT: ANSON, Donald S.
APPLICANT: ORSBORN, Annette M.
APPLICANT: CLEMENTS, Peter R.
APPLICANT: MORRIS, Charles P.
APPLICANT: MORRIS, Charles P.
APPLICANT: MORRIS, Charles P.
APPLICANT: MORRIS, Charles P.
APPLICANT: MORRIS, SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC TILE OF INVENTION: SEQUENCES ENCODING SAME
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/494,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: DIGGIGLO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 89782
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEPHONE: 516-742-436
TELEPHONE: 516-742-436
TELEPHONE: 616-742-436
TENGTHONE: 616-7
US-09-385-707-4/c; Sequence 4, Application US/09385707; Patent No. 6238662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
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Best Local Similarity
Matches 58; Conserva
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEPAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
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MOLECULE TYPE: DNA (genomic)
                                                                          Howson & Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4405 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWSON & 1
                                                                                                                Spring House
Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408..2789
 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                 STATE: Pennsylve COUNTRY: U.S.A. ZIP: 19477
                                                                                                                                                                                                                                                                                                                          FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-07-885-972A-3
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                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    465 GGGGCGGGGGCGGCGGCCGAGCCGAATCCCCTCCACCGGGACGCCCCGCTGCCGCTC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.4%; Score 29.6; DB 4; Length 2255; Best Local Similarity 61.8%; Pred. No. 11; Matches 47; Conservative 0; Mismatches 29; Indels 0
                                                                                        APPLICANT: SOCIAL AND ADDRESS.
APPLICANT: Donnelly, Robert
APPLICANT: Mariano, Thomas
APPLICANT: Cock, Jeffrey
APPLICANT: Emmanuel, Stuart
APPLICANT: Schwartz, Barbara
TITLE OF INVENTION: and its Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,572B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barr, Philip J.
Brake, Anthony J.
Kaufman, Rnadal J.
Tekamp-Olson, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-07-885-972A-3/c
'Sequence 3, Application US/07885972A
'Patent No. 5460950
'GENERAL INFORMATION:
Sequence 3, Application US/08871572B Patent No. 6287853
                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Muccino
STREET: 758 Springfield Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MUCCION, Richard R.
REGISTRATION NUMBER: 32,538
REFERENCE/POCKET NUMBER: UMD1-
TELECOMMUNICATION INFORMATION:
TELEFROM: (908) 273-4988
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                         Pestka, Sidney
Kotenko, Serguei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9-JUNE-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wasley, Louise
Wong, Polly A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2255 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             525 GGGAAGAGCGGGCCC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 ggggagctccgcgcac 98
                                                                                                                                                                                                                                                                                       ADDALL
STREET: /or
CITY: Summit
STATE: New Jersey
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                         GENERAL INFORMATION:
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US-08-871-572B-3
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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TITLE OF INVERTOR: Rethods of Use Thereof
NUMBER OF SEQUENCES:
CORRESPONDENCE NAME OF SEQUENCES:
CORRESPONDENCE NAME OF SEQUENCES:
CORRESPONDENCES:
CORRESPONDE
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APPLICANT: Brake, Anthony J.
APPLICANT: Brake, Anthony J.
APPLICANT: Raufman, Rnadal J.
APPLICANT: Teamp-Olson, Patricia
APPLICANT: Wasley, Louise
APPLICANT: Wong, Polly A.
TITLE OF INVENTION: Expression of PACE in Host Cells and
TITLE OF INVENTION: Mathods of Use Thereof
NUMBER OF SEQUENCES: 7

GENERAL INFORMATION:

STREET: Spring House Corporate Center, P.O. Box 457 CITY: Spring House

Pennsylvania

19477

COUNTRY:

Howson & Howson

CORRESPONDENCE ADDRESS: ADDRESSEE: Howson &

SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/480,382

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy

APPLICATION NUMBER: USCOB/480,382
FILING DATE: 07-UNN-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,092
FILING DATE: 20-MX-1990
APPLICATION NUMBER: US 07/621,092
FILING DATE: 26-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,859
FILING DATE: 29-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,443
FILING DATE: 29-NOY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,443
FILING DATE: 30-NOY-1990
PRIOR APPLICATION NUMBER: US 07/621,445
FILING DATE: 30-NOY-1990
ATTORNEY AGENT INFORMATION:

G15181A

NAME: Bak, Mary E. REGISTRATION NUMBER: 31,215 REFERENCE/DOCKET NUMBER: GI TELECOMMUNICATION INFORMATION: TELEPHONE: 215-540-9206

TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS: LENGTH: 4405 base pairs TYPE: nucleic acid

unknown

STRANDEDNESS: TOPOLOGY:

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APPLICANT: Wasley, Louise
APPLICANT: Wong, Polly A.
TITLE OF INVENTION: Expression of PACE in Host Cells and
TITLE OF INVENTION: Methods of Use Thereof
                                                                                                                                                         : Spring House Corporate Center, P.O. Box 457
Spring House
Pennsylvania
                                                                                                                                                                                                                       COUNTIAL

ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/745,880
FTI.NG DATE: 08-NOY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ELING DATE: 07-JUN-1955
APPLICATION NUMBER: US 07/885,972
FILING DATE: 20-MAY-1992
APPLICATION NUMBER: US 07/621,092
FILING DATE: 26-NOY-1990
PRIOR APPLICATION NUMBER: US 07/620,859
FILING DATE: 29-NOY-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/621,443 FILING DATE: 29-NOV-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/621,457 FILING DATE: 30-NOV-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: G15181A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-906
TELEFAX: 215-540-9018
INFORMATION FOR SEQ ID NO: 3:
                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWSON & HOWSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 4405 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
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408..2789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION:
US-08-745-880-3
                                                                                                                                                           STREET:
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275 GCTCGGGAGGGTGAAGAGTGCCGACCCCTGGGGAGCCCTGGCGGGAAACTTTTCCAGGC 216
                                                                                   7 gcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctcccgggc 66
                                                   ;
0
        Score 29.6; DB 2; Length 4405;
Pred. No. 14;
0; Mismatches 44; Indels 0
                                                                                                                                                                 67 tgcggcagggcagggcggggggggccccaccaacagag 106
                                                                                                                                                                                                    215 GACCGCGCGCGCGCTCGGCCCCTCGGCCGAGCGGAG 176
          13.4%;
56.0%;
Query Match
Best Local Similarity 56.09
Matches 56; Conservative
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Sequence 3, Application US/08480382

RESULT 11 US-08-480-382-3/c

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                                                                                                                   DB 2; Length 4405;
                                                                                                                 13.4%; Score 29.6; DB 2; Length 44C
56.0%; Pred. No. 14;
tive 0; Mismatches 44; Indels
                                                                                                                                                                                                                                                                   215 GACCGCCGCGCGCGCCCCTCGGCCGAGCGGAG 176
                                                                                                                                                                                                                                                  67 tgcggcagggcagggcggggagctccgcgcaccaacagag 106
MOLECULE TYPE: DNA (genomic)
                                                                                                                 Query Match 13.49
Best Local Similarity 56.09
Matches 56; Conservative
                                  CDS
408..2789
                                  NAME/KEY:
                                                   LOCATION:
                                                                 US-08-480-382-3
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                                                                                                APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Airkle, Ross
APPLICANT: Gyr, Devon
APPLICANT: Gyr, Devon
TILLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CUBRENT APPLICATION NUMBER: US/09/335,409
CURRENT APPLICATION NUMBER: US/09/335,409
SOFTWARE: PATENTION FOR SEQ. 10 Not. 2.0
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: FALCHIN Ver. 2.0
SOFTWARE: FOR SEQ. 10 Not. 2.0
SOFTWARE: FOR SEQ. 10 Not. 2.0
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APPLICANT: Schupp, Thomas
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Like, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4.30582A
CURRENT APPLICATION NUMBER: US/09/568,102
CURRENT FILING DATE: 2000-05-10
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SUFFRARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.8%; Score 29.6; DB 3; Length 68750;
Best Local Similarity 61.8%; Pred. No. 35;
Matches 47; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
13.4%; Score 29.6; DB 4; Length 68750;
Best Local Similarity 61.8%; Pred. No. 35;
Matches 47; Conservative 0; Mismatches 29; Indels 0;
                         Sequence 1, Application US/09335409
Patent No. 6121029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09568102
Patent No. 6346404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-335-409-1
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; ORGANISM: Sorangium cellulosum
US-09-568-102-1
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                                                                            GENERAL INFORMATION:
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LENGTH: 68750
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JS-09-335-409-1
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,480
CURRENT APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                 APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,969
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 61.8%; Pred. No. 35;
Matches 47; Conservative 0; Mismatches
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                        Sequence 1, Application US/09567969
Patent No. 6355457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09568480 Patent No. 6355458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-480-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Sorangium cellulosum
US-09-567-969-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Conservative
                                                                                                                 APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
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                                                                                             APPLICANT: Schupp, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                          GENERAL INFORMATION:
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US-09-567-969-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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- Oy 75 ggcagggggggggt 90 | | | | | | | | | | | | Db 18370 cgatcggcgaggtgct 18385

Search completed: September 20, 2002, 03:21:58 Job time: 14207 sec

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September 20, 2002, 03:14:51; Search time 5225.75 Seconds (without alignments) 636.716 Million cell updates/sec
                                                                                                                                                                                                                                                                                                  US-09-846-456-5
159
1 ttaatgaccagccacgggcg......tttcagaagaagacaaaca 159
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                    OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES
Result Query
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AX351033 Sequence AX351030 Sequence AX060713 Sequence AX060892 Sequence AX060719 Sequence AX060719 Sequence AX060898 Sequence AX06090 Sequence AX06090 Sequence AX06090 Sequence AX06090 Sequence AX06090 Sequence AX052948 Homo sapi AR258627 Homo sapi AR258624 Homo sapi AR258624 Homo sapi	AX139751 Sequence AX25277 Homo sapi AX253452 Sequence AX137830 Sequence AX139817 Sequence AX137831 Sequence AX127831 Sequence AX02230 Homo sapi AR024328 Homo sapi AR024328 Homo sapi AX092594 Sequence AX092594 Sequence AX15712 Sequence AX091466 Mus muscu AX5926 Mus muscul AX5926 Mus muscul AX5926 Mus muscul AR587265 Mus muscul	AF362377 Gallus ga Continuation (9 of AL353725 Human DNA AC102919 Mus muscu AX092843 Sequence AF287142 Mus muscu AX080494 Sequence AC087114 Mus muscu AC073805 Mus muscu AF328787 Homo sapi AX320362 Sequence	A linear PAT 06-FEB-2002 a; Vertebrata; Euteleostomi; ini; Hominidae; Homo. e,C., Naudin,L., Denefle,P., d Santamarina-Fojo,S. the abcl gene
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Dene
Brewer,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 2 08-NOV-2001;
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Atp binding cassette transporter protein abc1 polypeptides
Patent: WO 0078971-A 128-DEC-2000;
CV THERAPEGITICS, INC. (US)
Location/Qualifiers
Lawn, R.M., Wade, D. and Garvin, M. Regulation with binding cassette transporter protein abc1 Patent: WO 0079972-A 1 28-DEC-2000; CV THERAPEDIUS, INC. (US) Location/Qualifiers
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GWKLTQQOPYALLWRKLIARRSRKGFFAQIYLPAVFVCIALVFSI,YPPFGKYPSLE
LQPWWYNBQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQAGEEBW
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DILQDLTGRNISDLYWTYVQIIAKSLKNKTWYNERRYGGFSLGVSKYQALPSGEVN
DAIKOMKKHIKLAKDSSADRFLNSLGFFWTGLDTRNNVKWWFNNKGWHAISSFLNVIN
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QQLDGLDWTAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRTISRFMECVNLN
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FSWFISSLIPLLVAGALLVVILKGNKLEYSDPSVVEVELSYEAVVILQCFLISTLF
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HUMDEADVLGDRIATISHGKLCVGSSLFIKNQLGTGYYLTLYKRDVBSSLSCRNSS
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GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPAT
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MDPKARRFLWNCALSVVKEGRSVVLTSHSMEECEALCTRWAIMVNGRFRCLGSVQHLK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10442)
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Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA, complete cds.
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/protein.id="AAF98175.1"
/b_xref="G1:9755159".
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/chromosome="9"
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/codon_start=1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Lawn,R.M., Wade,D. and Garvin,M.
Regulation with binding cassette transporter protein abc1
Patent: WO 0078972-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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/db_xref="taxon:9606"
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1 (bases 1 to 10474)
Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abcl polypeptides
Patent: WO 0078971-A 7.8-DEC-2000;
CV THERAPEUTICS, INC. (US)
          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10474)
Lawn, R.M., Wade, D. and Garvin, M.

Lawn, R.M., Wade, D. binding cassette transporter protein abcl
Patent: WO 0078972-A 9 28-DEC-2000;

CV THERAPEUTICS, INC. (US)
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Pred. No. 1.1e-32;
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/organism="Homo sapiens"
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1 2305 c 2416 g 2843
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/db_xref="taxon:9606"
2304 c 2415 g 2844
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AX060898
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KEYWORDS
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 149034)

Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L.,
Cheng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschild,C.,
Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N.,
Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Santamarina-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A.,
Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E.,
Francois,T.L. and Brewer,H.B. Jr.
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Submitted (08-JUN-2000) Molecular Disease Branch, National
Institutes of Heath, National Heart, Lung and Blood Institute,
Bethesda, MD 20892, USA
Location/Qualifiers
1. 149034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 GAGCCACACGCTGGGCTGCTGGCTGAGGGAACATGGCTTGTTGGCCTCAGCTGAGGTTG 349
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Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abc1 polypeptides
Patent: Wo 0078971-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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Homo sapiens ABCAl (ABCAl) gene, complete cds.
AF275948
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Pred. No. 1.1e-32;
0; Mismatches 2;
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              DNA
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Sequence 9 from Patent WO0078971.
AX060900.
AX060900.1 GI:12406276
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a 2304 c 2415 g 2844
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1454. .148034
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7rpt_family="Alu"
5563. 5839
/rpt_family="Alu"
6615. 6877
/rpt_family="Alu"
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NK. IK. DGYWDPGPRADPEDMMY VWGGFAY LQDVVEQATIRVLTGTEKKTGYYWQQMPY
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TLAPVPQTIMDLEQNGWWYMQNPSPACQCSSDK TKMLEVCPRCAGGLEPPPRKKONTA
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DAXKQWKHLKLANGSSADRFINSLGRPWTGLDTRNNYKVWFNNKGWHAISSFLNYIN
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SPJ6. 313180
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Homo sapiens
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AF258627
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Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M. Compositions and methods for modulating hdl cholesterol and triglyceride levels
Patent: WO 0115676-A 108-MAR-2001; University of British Columbia (CA); Xenon Genetics Inc. (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25831 TTAATGACCAGGCGACGTCCCTGCTGTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCC 25890
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Pred. No. 1e-32;
0; Mismatches 2;
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/db_xref="taxon:9606"
37944 c 41170 g 54950 t
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67123. 67382
/rpt_family="Alu"
68499. 68731
                                     /rpt_family="Alu"
55297, .55344
/rpt_family="Alu"
58501, .58935
/note="LTR"
                                                                                                /rpt_family="HERV"
61246. .61480
                                                                                                                                    /rpt_family="Alu"
62812. .63077
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64082. .64306
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69481. .69760
 /rpt_family="Alu"
55029, 55000
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Best Local Similarity 98.7'
Matches 157; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 697)

8 Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.

Analysis of hakel gene 5' end: additional peptide sequence, promoter region, and four polymorphisms

L Biochem. Biophys. Res. Commun. 271 (2000) In press

E 2 (bases 1 to 697)

S Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.

Direct Submission

L Submitted (19-ApR-2000) Cardiovascular Research Institute, University of California, San Francisco, C.A. 94143-0130, USA
                                                                                                                                                                                                                                                                                                                                                             Homo saplens ATP binding cassette transporter 1 (ABCA1) mRNA, partial cds. AF258627
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/protein_id="AAF69513.1"
/protein_id="AAF69513.1"
/db_xref="G1:7769708"
/translation="MACWPQURILLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRL
SYPPYEOHEGHPWRAMPSAGTLEWWGIICNANNPCFRYPTPGEAPGVVGNFNKS"
198 c 190 g 156 t 1 others
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304 TTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCC 362
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Pred. No. 3.1e-29;
1; Mismatches 2;
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/db_xref="taxon:9606"
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1. .>697
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/gene="ABCA1"
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396. .>697
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Best Local Similarity 97.5%;
Matches 155; Conservative 1
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                                                                                     AF258623S2 200 bp DNA linear PRI 23-JUN-2000
Homo sapiens ATP binding cassette transporter 1 (ABCA1) gene, exon
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-JUN-2000) Cardiovascular Research Institute, University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 94143-0130, USA Sequence update by submitter
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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artificial sequence.
1 (bases 1 to 446)
Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
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Pullinger C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Anoizerat, B.E., Fielding, C.J. and Kane, J.P.
Analysis of hABCl gene 5' end: additional peptide sequence,
promoter region, and four polymorphisms
Biochem. Blophys. Res. Commun. 271 (2000) In press
2 (bases 1 to 200)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
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/db_xref="taxon:9606"
/chromosome="9"
/map="9431"
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PAT 30-MAY-2001
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1 (bases 1 to 446)

Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,H.B. and Dean,M.
Remaley,A., Brewer,H.B. and Dean,M.
Nucleics acids of the human abcl gene and their therapeutic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 gagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttg 120
Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H., Remaley,A., Brewer,H.B. and Dean,M.
Nucleic acids of the human abcl gene and their therapeutic and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 TTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 GAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTTGGCCTCAGCTGAGGTTG 211
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.4%; Score 142.2; DB 6 97.5%; Pred. No. 6.7e-29; Live 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                  Query Match 89.4%; Score 142.2; DB 6
Best Local Similarity 97.5%; Pred. No. 6.7e-29;
Matches 155; Conservative 0; Mismatches 3
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123 c 112 g 115 t
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                                                                      diagnostic application
Patent: WO 0130848 A 3 03-MAY-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic application
Patent: EP 1096012-A 3 02-MAY-2001;
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Sequence 3 from Patent EP1096012.
AX139751
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Location/Qualifiers
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Db 212 CTGCTGTGGAAGAACCTCACTTTCAGAAGAAGAAGAACA 250

Search completed: September 20, 2002, 03:15:13 Job time: 14027 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

September 20, 2002, 01:23:14; Search time 3895 Seconds (without alignments) 765.809 Million cell updates/sec Run on:

1 gtaattgcgagcgagagtga.....aacacaaaagtggaaaacag 221 US-09-846-456-4 221 Title: Perfect score: Sequence:

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

27472414 Total number of hits satisfying chosen parameters:

13736207 seqs, 6748477542 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:\* Database :

1: em\_estba:\*
2: em\_esthum:\*
3: em\_estin:\*
4: em\_estin:\*
5: em\_estov:\*
6: em\_estp:\*
7: em\_estro:\*
8: em\_estp:\*
10: gb\_est:\*
10: gb\_est:\*
11: gb\_htc:\*
12: gb\_gss:\*
12: gb\_gss:\*
13: em\_gss\_hum:\*
4: em\_gss\_lun:\*
5: em\_gss\_lun:\*
6: em\_gss\_lun:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AU135588 AU135588	AU121731 AU121731	Z44377 HSC1ZB081 n	BG678861 602624760	AZ769996 1M0571A17	BB657864 BB657864	BB665939 BB665939	BB594197 BB594197		BB568993 BB568993	BB570397 BB570397	BG384217 303216 MA	AL053013 Drosophil	BH470300 BOHMI69TR	AL065629 Drosophil	AL209545 Tetraodon	BB374442 BB374442
SUMMARIES	ΩΙ	AU135588	AU121731	244377	BG678861	AZ769996	BB657864	BB665939	BB594197	BB594265	BB568993	BB570397	BG384217	CNS0091P	BH470300	CNS006ON	CNS0200G	BB374442
	DB	6	σ	10	10	12	6	6	σ	6	σ	6	10	12	12	12	12	6
	Query Match Length DB	736	763	292	866	547	619	625	218	259	272	276	535	925	811	910	879	311
æ	Query	99.3	99.1	92.3	90.6	30.5	30.5	29.6	26.5	26.2	25.0	22.8	21.4	17.7	17.6	17.4	16.9	16.8
	Score	219.4	219	204	178.2	67.4	67.4	65.4	58.6	57.8	55.2	50.4	47.4	39.2	38.8	38.4	37.4	37.2
	Result No.	1	71	m	4	Ŋ	9	7	œ	თ	10	11	12	13	14	15	c 16	c 17

C76305 C76305 Mous AG127909 Pan trog1 BF237183 602028137 AG131276 Pan trog1 A1106381 Prosenbil	AG137074 Pan trog1 BB318923 BB318923 BI101161 602866848 AI850822 UI-M-BG1- AW489757 UI-M-BH3- AW490154 UI-M-BH3-	BE948350.UJ-M-BH3- BB698363 BB698363 BE943674 UJ-M-BH3- BE943841 UI-M-BH3- BE947468 UJ-M-BH3- BB696895 BB696895 AV334840 AV334840 BB547934 BB547934	AG073892 Pan trog1 BB317508 BB317508 BE692826 SAC338 MO BI082717 602877749 AA098273 mn94b09.r BB790023 BB790023 BF224565 uz19403.x BF319828 uy77e07.x AA562016 v121h01.r
0 C76305 2 AG127909 0 BF237183 2 AG131276 2 CNS0167			2 AG073892 BB317508 BB592826 0 BI082717 AA098273 BB790023 0 BF224565 0 BF319828
	1101000	466 10 476 9 489 10 489 10 557 9 650 9	
16.8 16.8 16.7 16.7	16.7 16.7 16.5 16.4	16.4 16.4 16.4 16.4 16.4 16.4 16.4	16.3 16.1 16.1 16.1 16.1 16.1 16.1
37.2 37.2 37 37 36.8	0 8 8 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9	22222222 26.22222 26.22222 26.22222 26.22222	88888888 88888888 8888888 9888888 9888888
c 20	00000 20000 300000		0 0 0 34 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0

## ALIGNMENTS

RESULT 1	
LOCUS	AU135588 124-OCT-2000 AU135588 PLACE1 Homo sapiens cDNA clone PLACE1002437 5', mRNA
ACCESSTON	
VERSION	M135588.1 GI:10996127
SOURCE	EST. human.
ORGANISM	Homo sapiens
REFERENCE	manumatia; buthella; Filmates; catarrnini; Hominidae; Homo. 1 (bases 1 to 736)
AUTHORS	ton a National V. Ishii, S., Saito, K., Kawai,
	Iammamoto,J., wakamatsu,A., nakamuta,I., nagai,I., sugamo,S. ama Isogai,T.
TITLE	HRI human cDNA project
JOURNAL	Unpublished (2000)
COMMENT	Contact: Takao Isogai
	Genomics Laboratory
	Helix Research Institute
	1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
	Tel: 81-438-52-3951
	Fax: 81-438-52-3952
	Email: genomics@hri.co.jp
	HRI human cDNA project; 5' - & 3' -end one pass sequencing: Helix
	Virology, Institute of Medical Science, University of Tokyo, and
	Helix Research Institute.
FEATURES	
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	/organism="Homo sapiens"
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BASE COUNT	163 a 199 c 199 g 170 t 5 others
ORIGIN	

61 GGGCTGCGGCAGGGCAGGGCGGGGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGC 120

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 763)

Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,

Tamamofo,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
                                                                                                                                                                                                                                     63 gggctgcggcagggcagggcagggcgcgcgcgcaccaacagagccggttctcagggcgc 122
                                                                                                                                                                                          61 CCGGCTGCGGCAGGCCGGGGAGCTCCGCGCACACAACAGAGCCGGTTCTCAGGGC 120
                                                                                                                                                             61 ccgggctgcggcagggcagggcgggggagctccgcgcaccaacagagccggttctcagggc 120
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                                                                               1 gtaattgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctc 60
                                                                                                                      1 GTAGTTGCGAGCGAGCGTGAGTGGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTC 60
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    Length 736;
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                                         1; Indels
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
                                                                                                                                                                                                                                                                                                                     181 ggggtaggagaaagagacgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                                                                                          181 GGGGTAGGAGAAGAGACGCAAACACAAAAGTGGAAAACAG 221
  DB 9;
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Best Local Similarity 100.0%; Pred. No. 6.9e-42;
Matches 219; Conservative 0; Mismatches 0;
99.3%; Score 219.4; DB 9 99.5%; Pred. No. 5.5e-42; tive 0; Mismatches 1
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205 c 260 g 158 t
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HRI human cDNA project
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Genomics Laboratory
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                                         Matches 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sednence.
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    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
SOURCE
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slite_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain;
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
3 others
                                                                                                                                                                                                                                                                       EST 14-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Buaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 292)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Rabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                       244377 292 bp mRNA linear EST 14-NOV-HSC12B081 normalized infant brain cDNA Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 caggggggggggctccgcgcaccaacagagccggttctcagggcgtttgctcttgttt 136
                                           121 TITGCICCTIGITITITCCCCGGITCIGITITCICCCCTTCTCCGGAAGGCTTGTCAAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single read.

Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-lzb08
Seq primer: (-21)Ml3_universal.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995) 95277534
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                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                             c-1zb08, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                      Z44377.1 GI:573506
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                                                                                                                                                                                                                                              BG678861 998 bp mRNA linear EST 01-MAY-2001 602624760F1 NCI_CGAP_SKn4 Homo sapiens cDNA clone IMAGE:4749735 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapbs-remain.in.in.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
CLone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAMMO603 row: g column: 16
High quality sequence stop: 860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="squamous cell carcinoma" / tab_nost="DH108 (Ti phage-resistant)" / hab_nost="DH108 (Ti phage-resistant)" / hote="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not!; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NoI_CGAP Library." 233 c 244 g 236 t
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NIH-WGC http://mgc.nci.nih.gov/.
                                   61 CAGGCGGGGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGGCGCTTTGCTCCTTGTTT 120
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/db_xref="taxon:9606"
/clone="IMAGE:4749735"
/clone_lib="NCI_CGAP_Skn4"
                                                                                                             180 GCAAACACAAAAGTGGAAAACAG 202
                                                                                                                                                                                                                                                                                                                     BG678861.1 GI:13910258
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Best Local Similarity 95.69
Matches 194; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 gplAR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. ooli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wen. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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GSS 16-FEB-2001
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mose whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
AZ769996 547 bp DNA linear GSS 16-FEB-20C 1M0571A17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0571A17 F, DNA sequence.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/db_xref="taxon:10090"
/clone="wcC1M6571A17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                 AZ769996.1 GI:12890721
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Best Local Similarity 62.4
Matches 138; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                                          Mus musculus
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Anakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Horii, F., Ishli, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Colazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M., and Hayashizaki, Y., Tanaka, T., Toya, T., Wuramatsu, M. and Hayashizaki, Y., et al. 2001)
                                                                                                                                                                                                                                                                             /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB665939 RIKEN full-length enriched, 2 days pregnant adult female oviduct Mus musculus cDNA clone E230023K11 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." 185 c 173 g 134 t l others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                      /clone_lib="RIKEN full-length enriched, 12 days embryo eyeball"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.5%; Score 67.4; DB 9; 62.4%; Pred. No. 4.2e-06;
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                                                                                                                                                                                                              /dev_stage="12 days embryo"
/lab_host="DH10B"
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                                 /db_xref="taxon:10090"
/clone="D230019D04"
                                                                                                                                                                                /tissue_type="eyeball"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 619)
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Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Rawai, J., Konno, H., Kouda

, M., Koya, S., Marsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,

Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Sano, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Janaka, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
Unpublished (2001)
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 1 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB657864 RIKEN full-length enriched, 12 days embryo eyeball Mus musculus cDNa clone D230019D04 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@goc.riken.go.jp,
URL:http://genome.goc.riken.go.jp,
URL:http://genome.goc.riken.go.jp,
URL:http://genome.goc.riken.go.jp,
URL:http://genome.goc.riken.go.jp,
URL:http://genome.goc.riken.go.jp,
W. Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNas to
Normalization and subtraction of cap-trapper-selected cDNas to
genes. Genome Res. 1.0 (10), 1617-1630 (2000)
wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Wadahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
'S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                              ccgggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggc 120
                                                                                                                                          85 CAGCGC-AAAGCTGGGCAGGGGGCGCCGCGGACCCGCCAACCACCGGCTTGGGGA 143
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26 GTAATTCCGAGGGCGAGCGAG-CGGGCCGGGACCGGCAGAGCCCACTTCTCTCCGCGGCG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                ggggtaggagaagagacgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                                                                                                                                                               204 GGGGTAGGGAAAACAGACTCAAACAGCAAAGTGGAAAACAG 244
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1. .619
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(11), 1757-1771 (2000)

(12), 2 and Hayashizaki,Y.

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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Tagawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikwa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki,Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.rlken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RIKEN full-length enriched, 2 days pregnant adult female oviduct"
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/dev_stage="2 days pregnant adult"
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62.1%;
                                                                                            81-45-503-9216
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Email: genome-resegac.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                            EST 30-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RIKEN full-length enriched, 4 days neonate thymus"
                                                                      120 TGCTCTGCTCCCTGTTTCCCCCCCACTTTTTTCTTCCCCTTTCTGGAAGGGTTTGTGCAGG 179
                                                                                                                                                                                                                                                                                                                                                                                                               BB594197 RIKEN full-length enriched, 4 days neonate thymus Mus musculus cDNA clone B630002C19 5', mRNA sequence.
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/dev_stage="4 days neonate"
/lab_host="DH10B"
/note="Site_1: Sal1; Site_2: BamH1; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                         183 ggtaggagaaagagacgcaaacacaaaagtggaaaacag 221
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/db_xref="taxon:10090"
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URL:http://genome.gsc.riken.go.jp,
carninci.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
.N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
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Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
                                                                                   system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RIKEN full-length enriched, 4 days neonate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.2%; Score 57.8; DB 9; Length 259; 57.1%; Pred. No. 0.00086; Live 0; Mismatches 92; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="thymus"
/dev_stage="4 days neonate"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="B630007C24"
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carhinci.P., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
                                                                                                     Alzawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodoyama, Y., Imotani, K., Ishii, Y., Itoh, W., Izawai, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Marayama, T., Miyazaki, A., Nakamura, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Sakaki, K., Sasaki, R., Sasaki, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Watahiki, A., Yamamura, T., Yasunishi, R., Yoshida, K., Yanishiki, A., Wuramatsu, M. and Haysshizaki, Y. Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched, 17 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer adapter of sequence [5
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/dev_stage="17 days embryo"
/lab_host="DH10B"
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/clone="3322401E06"
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Location/Qualifiers
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                                                                              REFERENCE
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1;

25.0%; Score 55.2; DB 9; Length 272; 58.0%; Pred. No. 0.0035; ive 0; Mismatches 83; Indels

Conservative

Best Local Similarity Matches 116; Query Match

ORIGIN

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Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus. 1 (bases 1 to 276)
Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hirozane, T., Hodoyama, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Myazaki, A., Nakamura, M., Nishi, K., Sakai, D., Sakai, P., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Watamatsu, M. and Hayashizaki, Y., Yasunishi, A., Wuramatsu, M. and Hayashizaki, Y. Yasunishi, A., Yoshida, K., RIKEN Mouse ESTS (Aizawa, K. et al. 2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome_res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carnindi,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Ltoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y.
Tomaru,Y., Carninci,P., Shibata,Y., All Hayashizaki,Y.
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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratoryy for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T-7.2 Suebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone="4222401021"
/clone_lib="RIKEN full-length enriched, 1 day pregnant
adult female mammary gland"
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Carninci,P. and Hayashizaki,Y.
                                                                                                                                                              cggggagctccgcgcaccaacagagccggttctcagggcgctttgctccttgtttttcc 141
                                                              79 GGCGCCGCGGGACCCGCGCAACCACAGCCGGCTTGGGGAACTGCTCTGCTCCTGTTTCC 138
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                                                                                                                               142 ccggttctgttttctccccttctccggaaggcttgtcaaggggtaggagaagagacgca
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                                                                                                                                                                                                                 The bases 1 to 535)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stonen, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2001)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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                                                                                                                                                                             contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [\,5\,'
                                                                           /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                          Division of Experimental Animal Research in Riken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CGCAAAGCTGGGCAGGGGGCGCCGCGGGATCCGCGCAACCACAACCGG--CTTGGGGAAC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 aattgcgagcgagagtgagtggggccgggacccgcagagccgagccgacccttctctccc 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.8%; Score 50.4; DB 9; Length 276; 55.0%; Pred. No. 0.048; ive 0; Mismatches 96; Indels 3
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BG384217
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PO Box 166, Clay Center, NE 68933-0166, USA
                /tissue_type="mammary gland"
/dev_stage="1 day pregnant adult"
/lab_host="DH10B"
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/sex="female"
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Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                            RIKEN.
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Web: www.genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                              /tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pGMV SPORT6; Site_1: XbaI; Site_2: XhoI;
/note="Vector: pGMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 925)
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                                                                                                                                                                                                                        /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                           /organism="Sus scrofa"
                                                                                                    Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1. 535
                    FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: G column: 13
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BOHMI69TR BOHM Brassica oleracea genomic clone BOHMI69, DNA
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
66 ctgcggcagggcagggcggggggggctccgcgcaccaacagagccggttctcagggcgcttt 125
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
122 c 178 g 270 t
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
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Town.C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSs: BOHMI69TF
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                                                                                                                                                              511 others
                                                                                                                                                                                                                                                                   68; Indels
                                                                   /organism="Drosophila melanogaster"
/db_xxef="Lexaon:7227"
/clone_lib="RPCI-98"
/clone="BACRI9D16"
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1. .811
/organism="Brassica oleracea"
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17.2%; Pred. No. 18;
tive 86; Mismatches
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/clone="BOHM169"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutooyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                             76 GGGAGTAGGAGTAGGTTTTAGGTTTTGCAAGGTCCACTCTGGCATCCCGTGCCGCA 135
                                                                                                                                                                                          71 gcagggcagggcagggagctccgcgcaccaacagagccggttctcagggcgctttgctcc 130
                                                                                                                                                                                                                                      136 GTACGCGTTTGTGGGTGCCACAATATCCCCACCTGCTGCAGCACATGTTGCACTTTACATC 195
                                                     Gaps
                                                                                             11 gcgagagtgagtgagtggggccggagccgcagagccgagccgaccttctctcccggggctgcg 70
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
    Score 38.8; DB 12;
Pred. No. 23;
0; Mismatches 97;
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18.9%; Pred. No. 28;
tive 80; Mismatches
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Nucleotide segmenc	Nucleotide sequenc	Nucleotide sequenc	Nucleotide segment	Nucleotide segment	Nucleotide sequenc	Human ABC1 genomic	Partial human ABC1	Human ABCA1 homolo
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dР	Query Match	1	98.0	98.0	98.0	98.0	98.0	98.0	96.4	89.4	89.4
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	10	42.	89.4	08	22	AAK52667	Himan poly	polynic Porti
	11	42.	6	7260	22	~		hinding
	12	42.	6	7260	22	AAI70315		ATP binding
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	14	42.	6	9741	22	AAS06120		DNA sed
	15	42.	6	9854	22	AAS06121	Human ABC1	DNA
	16	42.	9	10545	21	AAC69132	Human ABC1	dene
	17	40.	ω	736	22	AAH07432	Human cDNA	
	18	40.	œ	1556	22	AAH18606	Human cDNA	
	19	35.	S	7857	21	AAC69388	Human ABC1	cholest
	20	35.	S	7860	22	AAF83826	Human ABC1	
	21	35.	S	7860	22	AAF92835	Human ABC1	CDNA.
	22	35.	S	7861	21	AAC69387	Human ABC1	
	53	35.	S	7864	21	AAC69120	Human ABC1	cholest
	24	135.2	85.0	7864	21	AAC69385	Human ABC1	
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	56	35.	S	7864	21	AAC69389	Human ABC1	cholest
υ	27	'n.	2	50885	22	AAK70336	c	immune/haema
	28	J.	$^{\circ}$	37	22	AAF93084	ABC1 polymo	polymorphism
	59	35	2	298	21	AAC06182	Human secre	secreted pro
	30	m	2	23024	22	AAF25499	Nucleotide	sedneuc
	31		Н	534	21	AAC75311	Human ORFX	ORF866
	32	34.6	-	1133	22	AAD05589	Human secre	secreted pro
	33		0	5669	22	AAS08707	Human PD-A	PD-ATP-bindi
	34	٠	0	6522	22	AAS08706	Human PD-A	PD-ATP-bindi
	35		σ	6607	22	AAF54812	Nucleotide	sedneuc
Ö	36	31.4	9	8217	22	AAL07164	Human repro	reproductive
	37		σ	485	21	AAC01004	Human secreted	eted pro
	38		19.1	532	21	AAC01005	Human secre	secreted pro
	39		6	2043	18	AAT79627	Human Doc2	Doc2-beta qe
	40	30.2	9	1093	22	ABA08699	Human ESRPI	prot
U	41		σ	1727	21	AAC66225	Human cDNA	cDNA encodin
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<u> </u>	AAF	24680 8	AAFZ4680 standard; DNA; 10442	; DNA;	1044	2 BP.		
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Human; adenosine triphosphate binding cassette protein 1; ABC1; poblipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9q22-9q31; haart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                        Nucleotide sequence of a human ABC1 polypeptide.
                                                                                                                                              291..7076
/*tag= a
/product= "ABC1 polypeptide"
                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                               16-JUN-2000; 2000WO-US16765
                    20-APR-2001 (first entry)
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                                                                                                                  Homo sapiens
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                                                                                     Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                      The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) I polypetide. ABCI resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apoliopprotein-mediated mobilisation of intracellular cholesterol stores. ABCI is defective in Tangler disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 9422-941. The ABCI genes and proteins are useful for developing pharmaccutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, adenosine triphosphate binding cassette protein 1; ABC1; apoliopprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atheroscierosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 98.0%; Score 155.8; DB 22; Length 10442; Best Local Similarity 98.7%; Pred. No. 1.7e-36; Matches 157; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                           other disorders associated with hypercholesterolemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of a human ABC1 polypeptide.
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/product= "ABC1 polypeptide"
                                                                                                                                                            Disclosure; Page 122-128; 215pp; English.
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291..7076
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                               Garvin M;
(CVTH-) CV THERAPEUTICS INC
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                                                         WPI; 2001-137812/14.
                               Wade D,
                                                                                                                                   atherosclerosis -
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                              Lawn RM,
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The present sequence encodes a human adenosine triphosphate (ATP)

binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell

membranes and utilises ATP hydrolysis to transport a wide variety of

membranes and utilises ATP hydrolysis to transport a wide variety of

ubbtrates across the plasma membrane. ABC1 is a pivotal protein in

the apolipoprotein-mediated mobilisation of intracellular cholesterol

stores. ABC1 is defective in Tangier disease, a genetic disorder

characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is

localised to chromosome 9422-9431. The ABC1 genes and proteins are

useful for developing pharmaceutical agents for the treatment of heart

disease and other disorders associated with hypercholesterolemia and

atherosclerosis. The genes are useful for developing screening assays to

screen for compounds that regulate the expression of genes associated

with cholesterol transport. The genes and proteins are also useful for

are also useful as diagnostic indicators of cardiovascular disease and

other disorders associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 gagccacacgetgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttg 120
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                                                                                                                                                                                                                                                                                                 Garvin M;
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                                                              99US-0140264.
                                                                                         99US-0153872.
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16-JUN-2000; 2000WO-US16591.
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                                                              18-JUN-1999;
14-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that requlate the expression of genes associated with roblesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders
                                                                                                                                                                                                                                                                                                                                                                                                                 Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises
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                                                                                               /product= "defective ABC1 polypeptide"
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                                             Location/Qualifiers 323..7108
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99US-0153872.
99US-0166573.
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14-SEP-1999;
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                                               Key
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The present sequence encodes a human adenosine triphosphate (ATP)

binding cassette protein (ABC) 1 polypeptide, and is isolated from
a Tandjer disease patient. ABC1 resides in cell membranes and utilises
ATP hydrolysis to transport a wide variety of substrates across the
plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
mobilisation of intracellular cholesterol stores. ABC1 is defective in
Tandier disease, a genetic disorder characterised by abnormal
HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
9422-9431. The ABC1 genes and proteins are useful for developing
pharmaceutical agents for the treatment of heart disease and other
disorders associated with hypercholesterolemia and atherosclerosis. The
disorders associated with hypercholesterolemia and atherosclerosis. The
center the expression of genes associated with cholesterol
transport. The genes and proteins are also useful
as diagnostic indicators of cardiovascular disease and other disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
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                                                                 Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                   Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated moblisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccaggggctccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.0%; Score 155.8; DB 22; Length 10474; 98.7%; Pred. No. 1.7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "defective ABC1 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ctgctgtggaagaacctcactttcagaagaagacaaaca 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 170-176; 215pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CVTH-) CV THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawn RM, Wade D, Garvin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUN-2000; 2000WO-US16765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0140264.
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20-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     323..7108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-137812/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atherosclerosis
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                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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Matches 157; Conservative
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binding cassette protein (ABC) 1 polypeptide, and is isolated from
a Tangier disease patient. ABC1 resides in cell membranes and utilises

ATP hydrolysis to transport a wide variety of substrates across the
plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated

mobilisation of intracellular cholesterol stores. ABC1 is defective in
Tangier diseases, a genetic disorder characterised by abnormal

Tangier diseases, a genetic disorder characterised by abnormal

C angier disease, a genetic disorder characterised by abnormal

C plazmaceutical agents for the treatment of heart disease and other

G 422-9431. The ABC1 gene is localised to chromosome

942-9431. The ABC1 genes and proteins are useful for developing

C disorders associated with hypercholestrolemia and atherosclerosis. The

genes are useful for developing screening assays to screen for compounds

that regulate the expression of genes associated with cholesterol

A diagnostic indicators are also useful for are also useful

A diagnostic indicators are also useful for are also useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               indicators of cardiovascular disease and other disorders
                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of ABC1 polypeptide from Tangier disease patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
chromosome 9q22-9q31; heart disease; hypercholesterolemia;
atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; adenosine triphosphate binding cassette protein 1; ABC1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag* a
/product= "defective ABC1 polypeptide"
350 ctgctgtggaagaacctcactttcagaagaagacaaaca 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garvin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with hypercholesterolemia.
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                                                                                                                                                                                                         AAF24707 standard; DNA; 10474 BP
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99US-0153872.
99US-0166573.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUN-2000; 2000WO-US16591.
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                                                                                                                                                                                                                                                                                                                                                  (first entry)
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14-SEP-1999;
19-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                  20-APR-2001
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                                                                                                                                                                                                                                                                              AAF24707;
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                                                                                                                                                                         AAF24707
                                                                                                                                            RESULT
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DB 22; Length 10474;

Score 155.8; DB 2; Pred. No. 1.7e-36;

98.0%; 98.7%;

Query Match Best Local Similarity

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The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9922-9931. The ABC1 genes and proteins are useful for developing pharmacceutical agents. For the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
gagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttg 120
                                                                                 Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                                                                                                                                                                                                                                                                                                                                                                            Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
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/product= "defective ABC1 polypeptide"
                                                                                                                                  121 ctgctgtggaagaacctcactttcagaagaagacaaaca 159
                                                                                                                                                   Claim 30; Page 165-172; 211pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garvin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 323..7108
                                                                                                                                                                                                                                                  BP,
                                                                                                                                                                                                                                                  AAF24708 standard; DNA; 10474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUN-2000; 2000WO-US16591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0140264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawn RM, Wade D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB31367
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14-SEP-1999;
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                                                                                                                                                                                                                                                                                  AAF24708;
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genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 gagccacacgctggggggtgctggctgagggaacatggcttgttggcctcagctgaggttg 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                      1 ttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctccc 60
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                                                                                                                                                                                                                                                                               98.0%; Score 155.8; DB 22; Length 10474; 98.7%; Pred. No. 1.7e-36; 1.ve 0; Mismatches 2; Indels 0; (
                                                                                                                                                                                   Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with hypercholesterolemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRITISH COLUMBIA
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2000US-0213958.
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                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200115676-A2
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23-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UYBR-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-2001
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                                                                                                                                                                                                                                                                                   Query Match
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53229 ttaatgaccagccacnggcgtccctgctgtgagctctggccgctgccttccagggctccc 53288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; M, Arnould-Reguigne I, Prades C, Naudin L;
Jaye M, Searfoss GH, Remaley A, Brewer HB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents the partial coding sequence of human ABC1, which encodes amino acids 1-60 of the human ABC1 protein. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or
                                                                                                                                      9
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Human ABC1 protein, amino acids 1 to 60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
                            Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
                                                                                                                                     1 ttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctccc
                                                                           22; Length 183999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human ABC1 nucleic acids and polypeptides for treating
                                                                                                                                                                                                                                                                             53349 ctgctgtggaagaacctcactttcagaagaagacaaaca 53387
triglyceride level, and a cardiovascular disease
                                                                                                                                                                                                                                                          121 ctgctgtggaagaacctcactttcagaagaagacaaaca 159
                                                                         Score 153.2; DB 2
Pred. No. 2.1e-35;
                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atherosclerosis, malaria and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 167; 368pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
185..438
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Partial human ABC1 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                     BP
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                                                                         96.4%;
97.5%;
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01-MAR-2000; 2000US-0186260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                        Conservative
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                                                                                                                                                   WPI; 2001-316327/33.
P-PSDB; AAU02176.
                                                                        Query Match
Best Local Similarity
Matches 155; Conserv
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Lemoine C,
                                                                                                                                                                                                                                                                                                                                                                                                AAS04035;
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; oell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathkc; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological pathologies, and other diseases e.g. Tangier disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                                                                                                                                                                                                   152 gagccacacgctggggggggggctgaggggaacatggcttgttggcctcagctgaggttg 211
                                                                                                                                                                                                                                                                                        93 ttaatgaccagccac-ggcgtccctgctgtgagctctggccgctgccttccagggctccc 151
                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                                                                      1 ttaatgaccagccacgggggtcctggctgtcagctctggccgctgccttccagggctccc
                                                                                                                                                                                                                                                                                                                                 gagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttg
                                                                                                                                                                                                                ;
                                                                                                                                                                          DB 22; Length 446;
                                                                                                                                                                                                                Indels
                                                                                                                   Sequence 446 BP; 96 A; 123 C; 112 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ABCA1 homologue-encoding cDNA, SEQ ID NO:976.
                                                                                                                                                                        89.4%; Score 142.2; DB 22;
llarity 97.5%; Pred. No. 8.5e-33;
Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                           212 ctgctgtggaagaacctcactttcagaagaagacaaaca 250
                                                                                                                                                                                                                                                                                                                                                                                                       121 ctgctgtggaagaacctcactttcagaagaagacaaaca 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 833-835; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA09200 standard; cDNA; 7086 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pang YT, Liu C, Drmanac RT;
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27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                          Best Local Similarity
Matches 155; Conserv
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Sequences ABB10981-ABB12310 represent 1350 novel human polypeptides, and sequences ABB0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides.

Contibodies against the polypeptides, methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence to polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence to potential therapeutic applications. The polypeptides of the invention may differentiation activities; including cytokine, cell proliferation or cell fiferentiation activities; stam cell growth factor activity; has matopoiesis regulatory activity tissue growth activity; chemoclaticy activity, activin - or inhibbin-related activities; chemoclatic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncapenesis, cancer cell proliferation or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., mayeloid or lymphoid cell disorders) chronic inflammatory conditions (e.g., asthma or arthritis), cronary heart disease, arterial ischaemia, bone disorders (e.g., mayeloid or lymphoid cell conditions are proliferative metanoulatory activities may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound crepair or nucleic acids encoding them) may be used to promote vound tinger stam element of playerides manipulate stem cell growth factor activity may be used to neuroepithelial cells candered activity may be used to neuroepithelial continue manipulate stem cell growth factor activity may be used to neuroepithelial despector activi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ttaatgaccaggccacgggcgtccctgctgtcagctctggccgctgccttccagggctccc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel human polypeptide of the invention.
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Human; ATP binding cassette transporter 1; ABC1; coronary heart disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to four common polymorphisms in the gene encoding
                                                                                                                                                                         dermatological; atherosclerosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New adenosine triphosphate binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
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                                                                Human ATP binding cassette transporter 1 (ABC1) gene.
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/product= "Human ABC1 protein"
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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28-JAN-2002 (first entry)
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Best Local Similarity 97.55
Matches 155; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to erytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 ttaatgaccagccac-ggcgtccctgctgtgagctctggccgctgccttccagggctccc 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 gagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 gagccacacgctggggggggctgactggctgagggaacatggcttgttggcctcagctgaggttg 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides with cytokine-like activities useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 142.2; DB 22; Length
Pred. No. 1.7e-32;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ctgctgtggaagaacctcactttcagaagaagacaaaca 159
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                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2000; 2000US-0620325.
01-SEP-2000; 2000US-064936.
15-SEP-2000; 2000US-0663561.
20-CCT-2000; 2000US-0593325.
30-NOV-2000; 2000US-0728422.
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                                                                                                                                                                                                                                                                                                                                2000US-0560875.
2000US-0598075.
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                                                                                      WO200157190-A2.
                                                                                                                                                                                                                                                                                         03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
                     Homo sapiens.
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                                                                                                                                                          09-AUG-2001
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Tang YT, Zhao QA,

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Gaps

AAD21326;

AAD21326 RESULT

331

Query Match Best Local

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The present sequence is that of CDNA encoding the human adenosine triphosphate (ATP) binding cassette transporter 1 (ABC1) protein (see AMESO22). The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AAT70314, using an alternative ATC codon as initiation codon and thereby adding an extra 40 N-terminal amino acids to the encoded ABC1 protein (see AMESO228). The invention provides 4 common polymorphisms in the ABC1 gene. These were identified by sequencing the ABC1 gene in different Tangler kindreds. In the variant genes (numbering as in AAT70314), G is changed to A at position 596, T is changed to C at position 1136, A is changed to G at position 596, or any combination of these. All of these polymorphisms alter the amino acid sequence of ABC1 and therefore polymorphisms alter the amino acid sequence of ABC1 and therefore may affect its function. The 2 most common polymorphisms (G596A) and A258G9 are both associated with a decreased in vitro ApoA-I mediated efflux of cholesterol from mononuclear phagocytes, a feature typical of Tangler disease. (GHD) relative to GHD-free control subjects. The use of the provided ABC1 polymorphisms for the diagnosis and treatment of lipid disorders, cardiovascular control subjects. The use of the provided ABC1 polymorphisms for the diagnosis and inflammatory diseases (e.g. psoriasis, lupus
                                                                                                                                                                                                                                                                                                                             /*tag= b
/note= "alternative open reading frame of AAI70314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New adenosine triphosphate binding cassette transporter gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                      ATP binding cassette transporter 1; ABC1; human; lipid disorder; cholesterol; cardiovascular disease; inflammatory diseases; antiinflammatory; antilipeamic; antipsoriatic; dermatological; antiinflammatory heart disease; diagnosis; gene therapy;
                                                                      Human ATP binding cassette transporter 1 (ABC1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 26-28; 41pp; English.
                                                                                                                                                                                                                                                       Location/Qualifiers 321..7106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace(3836,C)
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                       replace(2969,G)
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                                                                                                                                                                                                                                                                                                                                                                   replace(976, A)
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                                    07-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                               /*tag= a
501..7106
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                                                                                                                                                                                  polymorphism; ss.
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                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                 variation
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AAI70315;
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ma Y;
                                                                                                                                                                                                                  229 ttaatgaccagccac-ggcgtccctgctgtgagctctggccgctgccttccagggctccc 287
                                                                                                                                                          1 ttaatgaccagccacgggggtccctgctgtcagctctggccgctgccttccagggctcc 60
         proteins by antisense or ribozyme technology or RNA decoys is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
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                                                                                             Query Match

89.4%; Score 142.2; DB 22; Length 7260;
Best Local Similarity 97.5%; Pred. No. 1.7e-32;
Matches 155; Conservative 0; Mismatches 3; Indels 1:
Modulation of ABC1 transcripts or
                                                       Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                                                                                                                                                                                                             Claim 1; Page 1086-1096; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polynucleotide SEQ ID NO 228.
                                                                                                                                                                                                                                                                                                                                                                                    AAK51683 standard; cDNA; 7281 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-0620325.
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15-SEP-2000; 2000US-0663561.
20-0CT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
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 erythematodes) is claimed.
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Yang Y,
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                 AAK51683;
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                                claimed
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production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prades C, Naudin L;
                                                                                                                     Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                                                                                                                                               9agccacacyctggycytgctggctgagggaacatggcatgttggcctcagctgaggttg 120
                                                                                                                                                                                                                                                                                                                                                               Brewer HB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
                                                                                                                                                                                                                             DB 22; Length 7281;
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Duverger N, Jaye M, Searfoss GH, Remaley A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes
                                                                                                                                                                             Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;
                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 89.4%; Score 142.2; DB 2 Best Local Similarity 97.5%; Pred. No. 1.7e-32; Matches 155; Conservative 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "Human ABC1 protein"
                                                                                                                                                  were missing at the time of publication.
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185..6967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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2000US-0186260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ABC1 DNA sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-316327/33.
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01-MAR-2000;
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Lemoine C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS06120;
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                                        The sequence represents the coding sequence #1 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological pathologies, and other disease e.g. Tangier disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Naudin L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s M, Arnould-Reguigne I, Prades C, Naudin L;
Jaye M, Searfoss GH, Remaley A, Brewer HB;
                                                                                                                                                                                                                                                                                                                                                                                                                     gagccacacgctgggcgtgctgactgaggaacatggcatgttggcctcagctgaggttg 120
                                                                                                                                                                                                                                                                                                                                                                                  93 ttaatgaccagccac-ggcgtccctgctgtgagctctggccgctgccttccagggctccc 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               152 gagccacacgctggggggggctgagggaacatggcttgttggcctcagctgaggttg
                                                                                                                                                                                                                                                                                        DB 22; Length 9741;
                                                                                                                                                                                                                                       Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                    89.4%; Score 142.2; DB 22;
97.5%; Pred. No. 1.8e-32;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Human ABC1 protein"
               Claim 1; Page 204-208; 368pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS06121 standard; cDNA; 9854 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosier-Montus M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-OCT-2000; 2000WO-EP10886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2000; 2000US-0186260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ABC1 DNA sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AVET ) AVENTIS PHARMA SA.
                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-316327/33.
P-PSDB; AAU02176.
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200130848-A2
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Lemoine C,
                                                                                                                                                                                                                                                                                                                    Matches 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS06121;
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New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes -
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Claim 1; Page 209-213; 368pp; English.

The sequence represents the coding sequence #2 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also baseful for treating and preventing acadiovascular and neurological pathologies, and other diseases e.g. Tangier disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes. 

Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;

Ĥ 1; Gaps Query Match

89.4%; Score 142.2; DB 22; Length 9854;
Best Local Similarity 97.5%; Pred. No. 1.8e-32;
Matches 155; Conservative 0; Mismatches 3; Indels 1;

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121 325 ò

Search completed: September 20, 2002, 03:09:36 Job time: 10645 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

September 20, 2002, 03:21:58 ; Search time 110.16 Seconds (without alignments) 354.536 Million cell updates/sec Run on:

US-09-846-456-5

1 ttaatgaccagccacgggcg..........tttcagaagaagacaaaca 159 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapor 1.0 Scoring table:

383533 seqs, 122816752 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
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6: /cgn2\_6/ptodata/2/ina/pcTUS\_COMB.seq:\* Issued\_Patents\_NA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 2, Appli	7	'n	'n	7		. ~	10,	7		7	7	7	7	'n	; ;	4	Τ,	, ,	,	Sequence 15, Appl	9	1	12.	1,	6	6
A	US-08-866-650-2	US-09-021-287-2	US-09-240-473-2	US-09-144-085-3	US-08-781-802-7	US-08-694-078-7	US-09-058-260-7	US-08-482-073-10	US-07-914-281-7	US-08-393-246-7	US-08-525-058A-7	US-08-696-731-7	US-09-042-531-7	US-08-482-385A-1	US-08-482-385A-5	US-09-422-869-1	US-08-646-981-4	US-08-640-906-1	US-09-395-936-1	US-09-422-869-7	US-09-082-092-15	US-08-911-321-6	US-09-103-840A-1	US-09-010-809-12	US-09-119-788-1	-08-673	US-08-614-877-9
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% Query Match	18.9	18.9	•	18.9	٠	18.5	18.5	18.0	18.0	18.0	18.0	18.0	•	17.6	17.6	17.5	17.4	17.4	17.4	17.4	17.2	17.2	17.2	17.1	17.1	17.1	17.1
Score	30	30	30	30	29.4	29.4	29.4	28.6	28.6	28.6	28.6		28.6	28	2	27.8	27.6	27.6	27.6	27.6	27.4	27.4	27.4	27.2	27.2	27.2	27.2
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	29, Appl		II. Appl	11, Appl	11, Appl	28, Appl	10, Appl	28, Appl	3, Appli	20, Appl	7, Appli	7, Appli	20. Appl	~	20, Appl	28, Appl	20, Appl	20, Appl	
	Seguence	Sequence 4	Sequence 1									Sequence							
	US-08-928-692-29	PCT-US91-00899-4	US-08-530-290-11	US-08-901-200A-11	US-09-219-391-11	US-07-841-646-28	US-07-901-703-10	US-08-147-023-28	US-08-206-864-3	US-08-278-729A-20	US-08-480-528A-7	US-08-479-666-7	US-08-155-343A-20	US-08-406-672-20	US-08-643-563A-20	US-08-447-570-28	US-08-643-763A-20	US-08-462-623-20	
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;	17.1	17.0	16.7	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	
	27.2	27	26.6	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4	
(	C 78	c 53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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; LOCATION: 611..3652
; OTHER INFORMATION: /product= "murine mTll protein"
US-08-866-650-2
                                                                                         APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Takahara, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
UNDMER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                   Sequence 2, Application US/08866650
Patent No. 5939321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4771 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 611..3652
                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
US-08-866-650-2
                                                                                                                                                                                                                                                                                                             STATE:
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Gaps 0; Query Match
18.9%; Score 30; DB 2; Length 4771;
Best Local Similarity 52.4%; Pred. No. 3.2;
Matches 66; Conservative 0; Mismatches 60; Indels

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Score 30; DB 4; Length 4771;
Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "murine mTll protein"
                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                     Sequence 2, Application US/09240473 Patent No. 6297011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BEFSON, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 9607
TELECHONE: 608-251-5000
TELEPHONE: 608-251-500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 4771 base pairs TYPE: nucleic acid minimumnesS: double
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52.4%;
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Best Local Similarity 52.4
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COCATION: 611..365;
COTHER INFORMATION:
US-09-240-473-2
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US-09-240-473-2
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                        63 gccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttgct 122
                                                                                                                3 aatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctcccga 62
  3 aatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctcccga
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                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Greenspan, Daniel S , APPLICANT: TAKAhara, Kazuhiko APPLICANT: Hoffman, Guy G APPLICANT: Hoffman, Guy G TITLE OF INVENTION: Mammalian Tolloid-Like Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELEPLOMMUNICATION INFORMATION:
TELEPLOME: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/021,287
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/866,650
FILING DATE:
                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09021287 Patent No. 5981717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
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52.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 4771 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 611..3652
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; OTHER INFORMATION:
US-09-021-287-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Greensp
                                                                                                                                                         123 gctgtg 128
                                                                                                                                                                                               261 GCTGAG 266
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US-09-021-287-2
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63 gocacacgetgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttgct 122
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) NAME/KEY: mat_peptide
; LOCATION: 245.1231
US-08-781-802-7
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-694-078-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
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                                                                 GENERAL INFORMATION:
APPLICANT: Gustafsson, Claes
APPLICANT: Gustafsson, Claes
APPLICANT: Ballech, Gary
APPLICANT: Julien, Bryan
APPLICANT: Julien, Bryan
APPLICANT: Julien, Bryan
TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND ENCODING DNA
TITLE OF INVENTION: THEREFOR
FILE REPERMORE: 30062-20020.20
CURRENT APPLICATION NUMBER: 05/09/144,085
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: 09/010,809
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 gecaegggegteettgetgteagetetggeegetgeetteeagggeteeegageeacaeg 70
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APPLICANT: ALENS, John
APPLICANT: FONSTEIN, Michael
APPLICANT: FONSTEIN, Wenchika
APPLICANT: DEMIRJIAN, David
APPLICANT: GASADABAN, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 32029 gtgggcgaagtggctggaagagcacggggaggtggggtggtcggacgtgg 32078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.9%; Score 30; DB 4; Length 33529; 54.5%; Pred. No. 5.8; tive 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 ctgggcgtgctgagctgagggaacatggcatgttggcctcagctgaggttg 120
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STREET: 300 S. Wacker Drive 32nd Floor
CITY: Chicago
STATE: 1111nois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/694,078
FILING DATE: 07-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/781,802
FILING DATE: 10-JAN-1997
CLASSIFICATION: 536
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                           Sequence 3, Application US/09144085
Patent No. 6280999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08781802
Patent No. 5969121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-144-085-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.55
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 33529
US-09-144-085-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 3
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LOCATION: 245..1231
OTHER INFORMATION: /note- "TspA E101 sequence longest
OTHER INFORMATION: open reading frame; other possible start codons are TTG/le
OTHER INFORMATION: TTG/leu13; TTG/leu15; GTG/val43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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APPLICANT: ALLEN, Larry
APPLICANT: ATKENS, John
APPLICANT: FONSTEIN, Michael
APPLICANT: VONSTEIN, Weronika
APPLICANT: DEMIRJIAN, David
APPLICANT: CASADABAN, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
18.5%; Score 29.4; DB 2; Length 3147;
Best Local Similarity 56.8%; Pred. No. 4.4;
Matches 54; Conservative 0; Mismatches 41; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff, Ltd. STREET: 300 S. Wacker Drive 7th Floor CITY: Chicago STATE: Illinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2858 GCGTACGCCAGGATGGGGCCCCGGTAAAGCCTTA 2892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 gcctcagctgaggttgctgctgtggaagaacctca 139
              PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/009,704
FILING DATE: 11-JAN-1996
PRICE AT 11-JAN-1996
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/001,995
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 95,963-E
TELEPHONE: 312-913-0001
TELEPHONE: 312-913-0001
TELEPHONE: 312-913-0001
TELEPHONE: 312-913-0001
TELEPHONE: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08694078 Patent No. 6218163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
12-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3147 base pairs
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APPLICANT: Hession, Catherine A.
APPLICANT: Hession, Catherine A.
APPLICANT: Lobb, Roy R.
APPLICANT: Coborn, Laurele
APPLICANT: Goelz, Susan E.
APPLICANT: Soborn, Laurele
APPLICANT: Rosa, Margaret D.
APPLICANT: Rosa, Margaret D.
TITLE OF INVENTION: MOLECULES (ELAMS) AND MOLECULES INVOLVED IN LEUKOCYTE
TITLE OF INVENTION: APPLESION (MILAS)
NUMBER OF SEQUENCES: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: cloned esterase OTHER INFORMATION: gene from bacteria E101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 29.4; DB 4; Length 3147; Pred. No. 4.4; 0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2858 gcgtacgccaggatgggggccccggtaaagcctta 2892
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US 90/02357
FILING DATE: 27-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/452675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1251 Avenue of the Americas
EARLIER APPLICATION NUMBER: 08/781,802
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: 08/827,810
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
: United States of America
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APPLICATION NUMBER: US/08/482,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: APPLICATION NUMBER: US 07/608298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-482-073-10/c
; Sequence 10, Application US/08482073
; Patent No. 6307025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.5%;
56.8%;
                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 56.8
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                       , NAME/KEY: CDS
, LOCATION: (245)..(1231)
US-09-058-260-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10020
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                                                                                                                                                                                   LENGTH: 3147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQ
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LOCATION: 245..1231
OTHER INFORMATION: /note= "TspA E101 sequence longest
OTHER INFORMATION: open reading frame; other possible start codons are TTG/leu9;
OTHER INFORMATION: TTG/leu13; TTG/leu15; GTG/val43"
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APPLICANT: Allen, Larry
APPLICANT: Allen, Larry
APPLICANT: Allen, Larry
APPLICANT: Allen, Larry
APPLICANT: Alkens, John
APPLICANT: Honstein, Weronika
APPLICANT: Demirjian, David
APPLICANT: Demirjian, David
APPLICANT: Demirjian, David
APPLICANT: Casadaban, Malcolm
TITLE OF INVENTION: Stable Blocatalysts for Ester Hydrolysis
FILE REFERENCE: 95-96-44
CURRENT APPLICATION NUMBER: US/09/058,260B
CURRENT FILING DATE: 1999-04-10
EARLIER APPLICATION NUMBER: 60/001,995
EARLIER APPLICATION NUMBER: 60/009,704
EARLIER FILING DATE: 1996-08-07
EARLIER FILING DATE: 1996-01-15
EARLIER PILING DATE: 1996-01-15
EARLIER PILING DATE: 1996-01-15
EARLIER FILING DATE: 1996-01-15
EARLIER PILING DATE: 1996-01-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29.4; DB 4; Length 3147; Pred. No. 4.4; 0; Mismatches 41; Indels 0
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                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,580
FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,704
FILING DATE: 10-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,995
FILING DATE: 07-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 95,963-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFRA: 312-913-0002
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTER STRICS:
LENGTH: 3147 base pairs
TYPE: NUCLEIC acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 08/694,078
EARLIER FILING DATE: 1996-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09058260B Patent No. 6218167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 18.5%;
Best Local Similarity 56.8%;
Matches 54; Conservative (
          07-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: mat_peptide
; LOCATION: 245..1231
US-08-694-078-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-09-058-260-7
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ANTI-SENSE: NO
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TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.0%; Score 28.6; DB 4; Length 2861; 57.1%; Pred. No. 7.5; tive 0; Mismatches 39; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
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NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEBRONE: (703)521-4500
TELERAX: (703)486-2347
TELEXX: 248855 OPAT UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 ccchacceacceacchageccceachage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 cacacgctgggcgtgctggctgagggaacat 95
                                                                                                                                                                                    NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFRENCE/DOCKET NUMBER: B124CIP4
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 596-9000
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2861 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/359516
FILING DATE: 01-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/914,281
FILING DATE: 19920720
CLASSIFICATION: 530
                                                                                                                 APPLICATION NUMBER: US 07/354151
FILING DATE: 28-APR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/07914281
Patent No. 5324663
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
FILING DATE: 18-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.15
Matches 52; Conservative
                                                                                          PRIOR APPLICATION DATA:
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ZIP: 22202
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US-08-482-073-10
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TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Alington
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28.6; DB 1;
Pred. No. 8;
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PREDICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-ULL-1992
ATTORNEY/AGENT INFORMATION:
NAME: LAVALIBER: 31,451
REGISTRATION NUMBER: 31,451
REGISTRATION NUMBER: 31,451
REFRENCE/DOCKET NUMBER: 2363-060-55
TELEPHONE: (703)521-4500
TEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1673 cccagccggcccgaccaggccccgggagcT 1643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08393246
Patent No. 5595900
GENERAL INFORMATION:
                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-07-914-281-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 18.0%;
Best Local Similarity 57.1%;
Matches 52; Conservative
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MEDIUM TYPE: Floppy disk
                                                                                   3647 base pairs
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       unknown
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                                                                      LENGTH: 3647 base p
TYPE: NUCLEIC ACID
STRANDEDNESS: unkno
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: U.S.A.
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MOLECULE TYPE:
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US-08-393-246-7

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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 52; Conserv
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                                                                                                                                                                                                                                                                                                                     Virginia
                                                                                                                                                                                                                                                                                                                                           U.S.A.
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MOLECULE TYPE:
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US-09-042-531-7/c
    US-08-696-731-7/c
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TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
NUMBER OF SEQUENCES: 23
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                                                                                                           1733 TGAGCTGGCCAGGACGCCCAACCGGCACCGCCCGTCCCTTTCTTCCACTGCGCCCGGGG 1674
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                                                 Gaps
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Alighon STATE: Virginia
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      Length 3647;
                                               Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,058A
                                             0; Mismatches 39;
Score 28.6; DB 1;
Pred. No. 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31.451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEFAX: (703)486-2347
TELEFAX: (703)486-2347
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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    18.0%;
57.1%;
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TYPE: nucleic acid
STRANDEDNESS: double
Query Match
Best Local Similarity 57.1<sup>st</sup>
Matches 52; Conservative
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APPLICANT: LOWE, JOHN B.
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Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                           US-08-525-058A-7/c
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TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIFIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                      ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REPERBENCE/DOCKET NUMBER: 2363-060-55
TELECOMUNICATION INFORMATION:
TELEPAX: (703)521-4500
TELERAX: (703)466-2347
TELEX.
TELEX. 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3647 base pairs
LENGTH: 3647 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-UUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 cacacgctgggcgtgctggctgagggaacat
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APPLICATION NUMBER: US/08/696,731
FILING DATE: 14-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/393,246
; Sequence 7, Application US/08696731; Patent No. 5955347; GENERAL INFORMATION: APPLICANT: LOWE, JOHN B.
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; Patent No. 6268193
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                                         TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLLPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
CORRESPONDENCE ADDRESS:
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Patent No. 5728561
GENERAL INFORMATION:
APPLICANT: DENOYA, CLAUDIO D.
TITLE OF INVENTION:
TITLE OF INVENTION: GENES ENCODING BRACHED CHAIN ALPHA
TITLE OF INVENTION: KETOACID DEHYDROGENASE FROM STREPTOMYCES SPECIES
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                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
                                                                                                                                                                                                                                         STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.0%; Score 28.6; Di
Best Local Similarity 57.1%; Pred. No. 8;
Matches 52; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 cacacgctgggcgtgctggctgagggaacat 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-UUL-1992
ATRONEY/AGENT INFORMATION:
NAME: LAVAILeye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 08/220,433
                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 3647 base pairs
                         LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
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TITLE OF INVENTION: KE'
NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>Q</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                        22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-482-385A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE:
US-09-042-531-7
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Satent No. 5/2000.
GENERAL INFORMATION:
APPLICANT: DENOYA,, CLAUDIO D.
TITLE OF INVENTION: GENES ENCODING BRACHED CHAIN ALPHA
TITLE OF INVENTION: KETOACID DEHYDROGENASE FROM STREPTOMYCES SPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 cgggcgtccctgctgtcagctctggccgctgccttccagggctcccgaggccacacgctgg 74
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0
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                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,385A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAM:
APPLICATION NUMBER: US/08/482,385A
FILLIG DATE: 07-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SHEYKA, ROBERT F.
REGISTRATION NUMBER: 31,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 gcgtgctggctgagggaacatggcatgttggcctcagctg 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 GCGTACAGGCGCCAGCAGTAGCGGGTCGGCCTCCGCGG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
ADDRESSEE: PETER C. RICHARDSON
STREET: 235 EAST 42ND STREET, 20TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: PETER C. RICHARDSON
STREET: 235 EAST 42ND STREET, 20TH FLOOR
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   PC8346C
                                                                                      COUNTRY: U.S.A
ZIP: 10017-5755
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08482385A Patent No. 5728561
                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: SHEKKA, ROBERT F.
REGISTRATION NUMBER: 31,304
REFERENCE/DOCKET NUMBER: PC83
TELECOMMUNICATION INFORMATION:
TELEPPHONE: 212-573-1189
TELEPHONE: 212-573-1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-573-1939
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1146 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.69
Best Local Similarity 55.09
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-482-385A-1
                                                                   NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NEW YORK COUNTRY: U.S.A ZIP: 10017-5755
                                           NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-08-482-385A-5/c
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REFERENCE/DOCKET NUMBER: PC8346C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-573-1189
TELEFAX: 212-573-189
TELEFAX: 212-573-189
TELEFAX: 212-573-189
TELEFAX: 212-573-189
TENGTH: 27-57-189
SEQUENCE CHARACTERISTICS:
LENGTH: 2728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-482-385A-5
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ô Query Match 17.6%; Score 28; DB 1; Length 2728; Best Local Similarity 55.0%; Pred. No. 11; Matches 55; Conservative 0; Mismatches 45; Indels 0; Gaps

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QQ

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Search completed: September 20, 2002, 03:22:05 Job time: 14214 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 01:23:18; Search time 3895 Seconds (without alignments)

Fithe: US-09-846-456-5

Sequence: 159

Sequence: 159

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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Database : EST:\*

1: em\_estba:\*
2: em\_esthum:\*
3: em\_estin:\*
4: em\_estru::\*
5: em\_estpl:\*
6: em\_estpl:\*
7: em\_estpl:\*
7: em\_estpl:\*
10: gb\_est:\*
11: gb\_tss:\*
11: gb\_sss:\*
13: em\_gss\_pln:\*
14: em\_gss\_pln:\*
15: em\_gss\_pln:\*
16: em\_gss\_vrt:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AU135588 AU135588	BB657864 BB657864	Z44377 HSC1ZB081 n	BG384217 303216 MA	AA914462 vz01f08.r	AV845237 AV845237	BH087817 RPCI-24-3	AQ848626 LMAJFV1_1	AV862022 AV862022	AW751638 RC5-CT007	BB843149 BB843149	BF484412 WHE2323_B	BE471178 WHE0285_G	BM149133 TCAAP2E63	BG325753 602424464	AV864011 AV864011	AV892280 AV892280	
	ID	AU135588	BB657864	244377	BG384217	AA914462	AV845237	BH087817	A0848626	AV862022	AW751638	BB843149	BF484412	BE471178	BM149133	BG325753	AV864011	AV892280	
	DB	6	6	10	10	σ	6	12	17	6	σ	σ	10	10	10	10	σ	6	
	Query Match Length DB	736	619	292	535	440	533	514	482	571	301	365	516	530	344	1574	571	579	
оP	Query Match	88.4	45.8	44.5	44.5	23.3	22.6	22.4	22.3	22.0	21.9	21.9	21.9	21.9	21.8	21.8	21.6	21.6	
	Score	140.6	72.8	70.8	70.8	37	36	35.6	35.4	35	34.8	34.8	34.8	34.8	34.6	34.6	34.4	34.4	
	Result No.	-	10	m	4	7.	, ve		. oc	6	10	11	12	3	14	. r.	15	c 17	

BH087727 RPCI-24-3 BG398045 602439575 AW313960 9668 MARC AQ885360 H25552_B BTEA1604 AFESO MA	BC675383 602622695 BF128237 601810479 BG747266 602704923 AL065132 Drosophil BB132336 BB132336	AL530607 AL530607 BB866093 BB866093 BB653232 BB653232 BG700305 602679956 BG717361 602689696 BITS421 602689696	HALOSBY A BARDOSBY A BARDOSBY A BARDOSBY B BIT70317 603056222 BG830641 602767253 B1653815 AL539815 AL539815 AQ452008 HS_5186_B	BE991503 UI-M-CG0P BB644307 BB644307 BE991359 UI-M-CG0P AQ745776 HS_2272_A AA726802 vu42h07.r
Æ	0 BL041094 0 BG675383 0 BF128237 0 BG747266 2 CNSO06DN	9 AL530607 9 BB866093 9 BB653232 10 BG700305 10 BG717361 10 B1915421	9 BB265873 9 BB265874 10 B1770317 10 BG830641 10 B1668321 9 AL539815 12 AQ452008	10 BE981503 9 BB644307 10 BE981359 12 AQ745776 9 AA726802
	5/5 10 791 10 1901 10 543 10 997 12			615 682 724 1 801 1 472
21.4 21.3 20.8 20.8	200.8 200.8 200.6	200.3 200.3 200.3 200.3	20.1 20.1 20.1 20.1 20.1	20.0 20.0 20.0 19.0
34 33.8 33	33 33 32.8 32.8	325.2 32.2 32.2 32.2 32.2	32 32 32 32 31,8	31.8 31.8 31.8 31.8
c 19 20 21		2 2 8 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	0 34 33 34 0 4 0 4	) 0

## ALIGNMENTS

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RESULT 1 AU135588 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE	ORGANISM	REFERENCE AUTHORS	JOURNAL	FEATURES SOUT	BASE COUNT ORIGIN

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MEDLINE
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                                 FEATURES
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-resegoc.riken.go.jp,
URL:http://genome.goc.riken.go.jp,
Carnici.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
A., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper.selected cDNAs to
prepare full:length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fuliwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
.K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB657864 Linear EST 26-OCT-2
BB657864 RIKEN full-length enriched, 12 days embryo eyeball Mus
musculus cDNA clone D230019D04 5', mRNA sequence.
                                                                                                                                                                                                                                                  222 TTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCC 280
                                                                                                                                                                                                                                                                                                                                  61 gagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttg 120
                                                                                                                                                                                                                                                                                                                                                                                                               281 GAGCCACACGCTGGGGTGCTGGCTGAGGGAACATGGCTTGTTGGCCCCAGCTGAGGTTG 340
                                                                                                          Gaps
                                                                                                                                                                     1 ttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctccc 60
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                                                                                                          1;
        88.4%; Score 140.6; DB 9; Length 736; 96.9%; Pred. No. 1.4e-28; Live 0; Mismatches 4; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ctgctgtggaagaacctcactttcagaagaagacaaaca 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 CTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB657864.1 GI:16491690
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                                                                                    Matches 154; Conservative
        Query Match
Best Local Similarity
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BB657864
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SOURCE

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/ntc="Site_nijos" //ntc="Site_nijos" /ntc="Site_nijos" /ntc="Site_nijos" /ntc="Site_nijos" /ntc="Site_nijos" /ntc="Site_nijos /ntc="Site=nijos /ntc=nijos /ntc=ni
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Auffray,C., Behar,G., Bols,F., Bouchler,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Poullot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                        /db_xref="taxon:10090"
/clone="b230019b04"
/clone_lib="RIKEN full-length enriched, 12 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 TTAATGACCAGCCAC-AGAGTCACAGCTCTGTGCTGGCTGCT-CCCTCCAGGGCTCTC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 gagccaca-----cgctgggggtgctgagggaacatggcatgttggcctcag 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genethon Centre de recherche sur le Genome Humain
1,rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
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45.8%; Score 72.8; DB 9; Length 619;
Best Local Similarity 77.4%; Pred. No. 5.9e-10;
Matches 130; Conservative 0; Mismatches 27; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="12 days embryo"
/lab_host="DH10B"
                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="eyeball"
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Location/Qualifiers
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/tissue_twpe="total brain"
/dev_stage="3 months old"
/dev_stage="3 months old"
/note="corgan: brain, vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=mmscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dn) primed and directionally
cloned 5 -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press" 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
1 (bases 1 to 535)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 TTAATGANCAGCCAC-GGCGTCCCTGCTGAGCTCTGGCCGCTGCCTTCCAGGGNTCCC 264
                                           Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-1zb08 Seq primer: (-21)M13_universal.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctccc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.5%; Score 70.8; DB 10; Length 292; 94.3%; Pred. No. 1.7e-09; Live 0; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG384217 535 bp mRNA linear 303216 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence. BG384217
                                                                                                                                                                                                                     /clone_lib="normalized infant brain cDNA"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
T=1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-1zb08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: G column: 13
Seq primer: ATTTAGGTGACATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
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Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.37
Matches 83; Conservative
                         Single read.
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VERSION
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                                                                                                   FEATURES
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AA914462 440 bp mRNA linear EST 14-APR-1998 vz01f08.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1314471 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gasels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwook,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                        /clone_lib="MARC IPIG"
/tissue_type="pooled"
/tab_host="DHIOB"
/note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                       54 ggctcccgagccacacgctggcgtgctgagctgagggaacatggcatgttggcctcagct 113
                                                                                                                                                                                                                                                                                                                                                                                                                244 GGAGCCACACGCAGGCTGGTGGTGCCAGCTGAGGTAACATGGCTTATTGGACTCAACT 303
                                                                                                                                                                                                                                                                                                                          0; Gaps
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                               Length 535;
                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
/db_xre="taxon:10090"
/clone="IMAGE:1314471"
/clone=lib="Soares_mammary_gland_NbMMG"
                                                                                                                                                                                                                                                                          Score 70.8; DB 10;
Pred. No. 2e-09;
0; Mismatches 22;
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High quality sequence stop: 439.
Location/Qualifiers
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/dev_stage="4 weeks"
/lab_host="DH10B"
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The WashU-HHMI Mouse EST Project
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/organism="Sus scrofa"
/db_xref="taxon:9823"
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Class: BAC ends
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I 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
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Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 533)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="rcieg08c18"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
/tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 ccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttgctg 123
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                                                                                                                                                                                                                                                                              148 cecrecescencaaecereceeerererecaarecrireceeeeerecaaecereeee 89
                                                                                                                                                                                                                                                                                                                  82 ggctgagggaacatggcatgttggcctcagctgaggttgctgctgtggaagaacctc 138
                                                                                                                                                                                                                                                                                                                                    88 TGACGAGTGAACACCTGAGGTCGGGTTCAGCAGAACTCCCGGGTGAAGAGGCCC 32
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                                                                                                                                                                         Score 37; DB 9; Length 440;
Pred. No. 3.8;
0; Mismatches 50; Indels
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                                                                                                        1 others
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/db_xref="taxon:7719"
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
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Department of Zoology
Kyoto University
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                                                                                        Bonaldo."
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Matches 67; Conservative
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Best Local Similarity
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Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 382 row: O column: 9
Seq primer: SP6
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BHO87817 514 bp DNA linear GSS 18-JUL-2001
RPCI-24-38209.TJ RPCI-24 Mus musculus genomic clone RPCI-24-38209,
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Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0200
Fax: 301 838 0200
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/note="Vector: pTARBAC1: Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."
                                                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 514)
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Pred. No. 9.5;
0; Mismatches
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/clone="RPCI-24-38209"
/clone_lib="RPCI-24"
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60.2%;
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AV862022.1 GI:16849546
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Mammalia; Eutheria;
1 (bases 1 to 301)
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                                                                                          Ciona intestinalis
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N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major Friedlin strain VI genome by shotgun sequencing' and the Washington University Genome Sequencing Center For Information on obtaining clone material please contact: Natalia S. Akopyants Ph.D. (natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D. Seq primer: -40UP from Gibco
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                                                                                                                       Akopyants, N. S., Clifton, S. W., Martin, J., Pape, D., Wylie, T., Li, L., Kissinger, J., Roos, D. S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, J., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Harvey, N., McCann, R., Tsagareishvili, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S. M. A survey of the Leishmania major Friedlin strain VI genome by shotgun sequencing: a resource for DNA microarrays and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="LMAJFV1_im12d06"
/clone_lib="Leishmania major FV1 random genomic library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 AGGCTCTGCCGTCGCAGCTTGCAGCACTTGAAGCAGCACGTCAGCGCCGCGGGGTGCCTGGG 290
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                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library construction: Natalia S. Akopyants, Ph.D
                                                                                                                                                                                                                                                                                                    Mol. Biochem. Parasitol. 113 (2), 337-340 (2001)
21192569
                                                                                                                                                                                                                                                                                                                                                       Other GSSs: lm12d06.yl
Contact: Akopyants, NS / Beverley, SM
WashU Leishmania Project
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/db_xref="taxon:5664"
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Pred. No. 11;
O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.3%;
57.8%;
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                      Leishmania major.
                                            Leishmania major
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FEATURES

ORIGIN

08-NOV-2001

AV862022 Nori Satch unpublished cDNA library, egg Clona intestinalis cDNA clone rcleg31005 3', mRNA sequence.

DEFINITION AV862022/c

RESULT

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AW751638 301 bp mRNA linear EST 28-APR-2000 RC5-CT0071-041099-002-g07 CT0071 Homo sapiens cDNA, mRNA sequence. AW751638
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="reacon:719"
/clone="rcieg31005"
/clone=lip="Nori Satch unpublished cDNA library, egg"
/tissue_type="whole animal"
/dev_stage="egg"
/ lif c 99 g 201 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 ccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttgctg 123
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                                                   1 (bases 1 to 571)
Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                             Email: satoh@ascidian.zool.kyoto-u.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Ciona intestinalis"
                                                                                                                                                                                                                                                                          Sākyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 ctgtggaagaacctcactttcagaagaagacaaaca 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                          Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Tagawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                   RİKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preparation of the wheat spike condition of the wheat Unbulished (2000).

Triticeae; Triticum.

(bases 1 to 516)

Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han Anderson, O.D., Chao, Y., Lazo, G.R., Miller, R., Rausch, C.J., Saaton, C.L. and Tong, Y.C. The structure and function of the expressed portion of the wheat Unpublished (2000)

Contact: Olin Anderson
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WHE2323_B07_D132S Wheat pre-anthesis spike cDNA library Triticum
aestivum cDNA clone WHE2323_B07_D13, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched, 6 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 gggcgtgctggctgagggaacatggcatgttggcctcagctgaggttgctgctgtggaag 132
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114 c 96 g 75 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="F430009P04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 aacctcactttcagaagaagacaaac 158
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BF484412.1 GI:11567713
     1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Tto, M., Kawai, J., Kolina, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okio, Saito, R., Sakai, C., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Tayanishi, A., Watahiki, A., Watahiki, A., Watahiki, A., Muramatsu, M., and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB843149 365 bp mRNA linear EST 26-NOV-2001 BB843149 RIKEN full-length enriched, 6 days neonate spleen Mus musculus cDNA clone F430009P04 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: colon; Vector: puc18; Site_1: Smal; Site_2: Smal; A min1-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196 / T16 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-CT0071-041099-002-g07&t3=1999-10-04&t4=1)
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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/db_xref="taxon:9606"
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70 c 85 a
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High quality sequence stop: 64.
Location/Qualifiers
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/dev_stage="Adult"
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                                         Tel: +55-11-2704922
Fax: +55-11-2707001
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US Department of Agriculture, Agriculture Research Service, Pacific
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US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_lost="E. coli Solm"
/lab_lost="E. coli Solm"
/lote="Vector: lambda Uni-ZAP XR, excised phagemid;
site_l: EcoRi; Site=2: xhol; plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ close lab (choi, close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 CGCCGCTGCCGACATCTCCGACCCATGACGAGCTCCAGATCAAGACAGATGTGCGGCAG 335
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                                                                                                                                                                                                                                 Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.

1. Statagene SK primer.

1. .516
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Pred. No. 16;
0; Mismatches 47; Indels 0:
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800 Buchanan Street, Albany, CA 94710, USA
TTE: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE2323_B07_D13"
                                                                                                                                                                                                    Email: oandersn@pw.usda.gov
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/note="Vector: Lambda Uni: 2AP XR, excised phagemid;
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temperature on filter paper with water, nystafin and
cefotaxime in covered crystallization dishes. Five-day old
seedlings were incubated for one day at 90% RR. After
removing endosperm, seedlings were transferred to
desiccator jar containing saturated MgSO4 at room
temperature for 24 hr. The tissue, total RNA, and poly(A)
RNA were prepared, a cDNA library was made, and the cDNA
clones were in vivo excised to give pBluescript phagemids
in the TJ Close lab (Choi, Close, Fenton) at the
University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 344)
Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr.,
Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
Pediarric Leukemia cDNA Sequencing Project (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 CGCCGCTGCCGACATCTCCGACCCATGACGAGCAGCTCAGTCAAGACAGATGTGCGGCAG 334
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Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratgene SK primer.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 gctggctgagggaacatggcatgttggcctcagctgaggttgctgctgtg 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 GGGAGAAAAGGAAGATTGGGATGCCGGCATCATCTCTGGACGCCGCTGTG 384
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BM149133.1 GI:17170474
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Best Local Similarity
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BM149133
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                                                                                                                                                                    1574 bp mRNA linear EST 27-FEB-2001
602424464F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4562559 5',
mRNA sequence.
                                                 /clone_lib="Pediatric acute myelogenous leukemia cell (FAB
M1) Baylor-HGSC project=TCAA"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1574)
NIH-MGC http://mgc.nci.nih.gov/.
NiH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapDs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCML274 row: p column: 16
High quality sequence start: 5
High quality sequence stop: 178.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34.6; DB 10; Length 344; Pred. No. 16; 0; Mismatches 19; Indels 0;
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Best Local Similarity 70.8%;
Matches 46; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                             57
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TITLE
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/organism="Homo sapiens"

source

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/clone="IMAGE:456259"
/clone="IMAGE:456259"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1216 TCACGAGCCCCCCTTGTGTTCCCGCTGGGCGCTCTTTCCGCTGGTGCCCTTGTGCCCCGG 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 taatgaccagccacggggggtccctgctgtcagctctggccgctgccttccagggctcccg 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 1574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 21.8%; Score 34.6; DE Best Local Similarity 55.4%; Pred. No. 25; Matches 67; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: September 20, 2002, 01:23:20
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Sequence:

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Run on:

Scoring table:

Word size :

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Database :

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P.,
Rosier-Montus, M.F., Remaley, A. and Santamarina-Fojo, S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 1 08-NOV-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
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Sequence 1 from Patent WO0183746.
AX351029
AX351029.1 GI:18616385
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AF287263
AC107969
                    AX351031
AF287262
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AC012230
HSA252201
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AX060713
AX060892
                                                                                                                                                                                AX060715
AX060894
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AX253452
AX351032
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AX127831
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AX060719
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AC021345
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100.0 3231

89.5 2893

54.1 201144

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S. Regulatory nucleic acid sequences of the abcl gene Patent: WO 0183746-A 3 08-NoV-2001;
Aventis Pharma S.A. (FR)
                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                        AF287262 201144 bp DNA linear PRI 29-APR-2001 Homo sapiens ATP-binding cassette 1 sub-family A member 1 (ABCA1) and SNAP protein genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-JUL-2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="ATP-binding cassette 1 sub-family A member 1" 33931. .18457 /gene="ABCA1" 33931. ,34151
                                              Qiu,Y., Cavelier,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F. Human and mouse abcal comparative sequencing and transgenesis
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Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
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Genomics 73 (1), 66-76 (2001)
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58319. .58476
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TITLE
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AUTHORS
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GOLGGLOWFATADDIVAFLAKHPEDVQSSNGSVTWREAFNETANDAIRTISRFMECVNLN
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NKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVVEQALIRVLTGTEKKTGVYMQMPY
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HHWDEADVLGORIAILSHGKLCCVGSSED-ELKRUGGGTGTYTLTJKKVDVSSLSSCRNSS
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LQPWMYNEQYIFVSNDAAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQAGEEBW
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GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPAT
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DAIKQMKKHLKLAKDSSADRFLNSLGRFWTGLDTRNNVKVWFNNKGWHAISSFLNVIN
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SASFVVELJOGENSKAKHLOFISGVEPYIWIEDENVEVPATLYVIIFICFOO
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TFVLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDMYKNQAMADALEREGENRFVS
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QNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSKKHVKAEMEQMALDVGLPSSKLKSKT
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exon exon exon exon exon exon exon exon	Query Match  Best Local Similarity 100 Matches 1749; Conservative

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aacaggogcccgccaccacatctggctaatttttgtattttagtaaagactgggtttca 1143
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                                                                                                                                                                                                                                                                                                                                            tttttcttgacacggagtcttgctctgtcactcaggctggagtgcagtggcatgatctcg 1023
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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Chassa 1 to 149034)

Santamarina-Fojo,S., Peterson,K., Knapper,C., Oiu,Y., Freeman,L.,

Cheng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschild,C.,

Prades,C., Chinin,G., Blackmon,E., Francois,T., Duverger,N.,

Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
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                                                                                132389 TCCAGAATTCCTTGCCTGGTGGCCTCCACATGCACTTCCAGGGCCTGCTTGGGCCTCTTC 32448
                                                                                                                                                                                                                                                                                                                                                                                     32149 AACAGGCGCCCCCCCACCATCTGGCTAATTTTTGTATTTTAGTAAAGACTGGGTTTCA 32208
                           tecagaatteettgeetggtggeetecacatgeaetteeagggeetgettggggeetette 1383
                                                                                                                                                                                                                                                                                                                gootggagatootgttgaotgtagoatggagggggttgtgcagotgaatgtotgcatgc 1503
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Santamarina-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A.,
Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E.,
Francois,T.L. and Brewer,H.B. Jr.
                                                                                                                                                                                                                                                                                                                            agggcaaacagtccatggtgcaaaggggccatgccacccagagttatgagtacctgggac
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Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
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AF275948
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Submitted (08-JUN-2000) Molecular Disease Branch, National Institutes of Heath, National Heart, Lung and Blood Institute, Bethesda, MD 20892, USA
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    149034
    organism="Homo sapiens"

                                                                                                         Location/Qualifiers
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25038. .???!
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NKTKOKYWPOPERADPFEDMRYWGGFRYLOPVOALIRVITGTEKKTGVYMOOMPY
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DGTLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESRETDLLSGMDGKGSYQVK
GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLE
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TATAVPQTIMDLEQNGNWTWONPSPACCSSOKIKKMLPVCPPGAGELEPPDRKONTA
DILODLTGRNISDY TYYQJIAKSIKNK IRVNEFRYGGFSLGVSNYOALPESQEVN
DAXKQMKKHLKLAKDSSADRFLNSLGRFWTGLDTRNNVKWFNNKGWHAISSFLNVIN
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PASFVVFLIQERVSKAKHLQFISGVKPVIYMLSNFVMDMCNYVVPATLVIIFICFQQ
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SWSDMRQEVMFLTNVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALF
GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPAT
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QNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVGLPSSKLKSKT
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STVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVEDIGHEL
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PLSWDLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQ
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NLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP
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NRFGDGYTIVVRIAGSNPDLKPVQDFFGLAFPGSVXKEKHRNMLQYQLPSSLSSLARI
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aattttacacgactgcaattctctggctgcacttcacaaatgtatacaaactaaatacaa 2040
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0; Mismatches
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99.8%;
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Direct Submission

Direct Submission

Submitted (11-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

on Jan 15, 2002 this sequence version replaced gi:18121468

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; Sw; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 mapping Group.
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                                                                                                                                                                                                                                                                                                                                                                PRI 11-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                96717 bp DNA linear PRI 11-JAN-2005 sequence from clone RP11-217B7 on chromosome 9, complete
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RP11-217B7 is from the library RPCI-11.1 constructed by the group
Of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1681 GCCTCCCAGTGACTTACTTGGGCGTTATTGTTTTGGAGGCCCAAGGAGGCTTCGGG 1740
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Institutes of Heath, National Heart, Lung and Blood
Institute, Bethesda, MD 20892, USA."
                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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3238. .3278
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AL359182.20
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Human DNA sequence.
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       /note="Sequence from overlapping clone RPI1-122F10 (AC026643). Assembly confirmed by restriction digest." 92050. 92163
/note="Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
                                                                                92411... 92557
/note="Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
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99.78;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M. Compositions and methods for modulating hdl cholesterol and triglyceride levels
Patent: WO 01156/6-A 1 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (C Location/Qualifiers
                                                                          18594 GAAGTAGGCTTGGGGCAGCTCTCTCATGCCACCTCATTCTGGCCAAAACTCAGGTCAAAC
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37944 c 41170 g 54950
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/organism="Homo sapiens"
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Sequence 1 from Patent WO0115676.
AX092589
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Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo. sapiens, clone RP11-1M10
1202 teccaaagtgetgggattacaggeatgagecaetgegeceageteagatecatecette 1261
                                                                                                                                                                                                                                                          1262 taagggcaaacagtccatggtgcaaaggggccatgccacccagagttatgagtacctggg 1321
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Submitted (21-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 22, 2000 this sequence version replaced gi:6454033. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                          Center clone name: 1.M.10

Center clone name: 1.M.10

Sequencing vector: M13, M77815, 100% of reads
Sequencing vector: M13, M77815, 100% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 14574 bases at least Q40
Consensus quality: 14574 bases at least Q20
Insert size: 178500; agarose-fp
Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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contig of 1707 bp in length
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22587: contig of 2356 bp in length
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contig of 2377 bp in length
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45448: contig of 2513 bp in length
48: gap of 100 bp
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2735 4415: cont
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31338: cont
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45449 45548: gap of

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117308 117407: gap of 100 bp 117408 124080 124179: gap of 100 bp 124080 124179: gap of 100 bp 124180 131281: contig of 6672 bp in length 131282 131381: gap of 100 bp 131282 131381: gap of 100 bp 131382 138059: contig of 6678 bp in length 131860 138159: gap of 100 bp 138060 138159: gap of 100 bp 145492 145591: gap of 100 bp 145592 157391: contig of 7332 bp in length 145592 157391: contig of 11800 bp in length 157392 157491: gap of 100 bp 157392 157491: gap of 17573 bp in length.
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88220: contig of 6007 bp in length

88320: gap of 100 bp

93499: contig of 5179 bp in length
                 48216: gap of 100 bp 52618: contig of 4402 bp in length 52718: gap of 100 bp 55592: contig of 3874 bp in length
                                                                                                      56692: gap of 100 bp
59635: contig of 2943 bp in length
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63661: contig of 3926 bp in length
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82113: contig of 5125 bp in length
48116: contig of 2568 bp in length
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13: gap of
88220: r
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71458: cont
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2490 tttagaggaagcaaattccactggtgccttggctgccgggaacgtggactagagtct 2549
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Eukaryotz, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases I to 1167)

Porsch-Ozcurumes, M., Langmann, T., Heimerl, S., Borsukova, H., Kaminski, W.E., Drobnik, W., Honer, C., Schumacher, C. and Schmitz, G. The zho finger protein 202 (znf202) is a transcriptional repressor of atp binding cassette transporter al (abcal) and abcgl gene expression and a modulator of cellular lipid efflux
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                3498 GGGCCGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCC 3557
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HSA252201 1167 bp DNA linear PRI I Homo sapiens partial ABC-1 gene for ATP-binding cassette transporter-1, 5'UTR and promoter region.
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/chromosome="9"
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1. .1167
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1. .1167
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Submitted (20-ARR-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
3 (bases 1 to 1167)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
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Submitted (23-UN-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
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On Jun 23, 2000 this sequence version replaced gi:7769713.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Regulation with binding cassette transporter protein abcl
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1643)
Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
Arp binding cassette transporter protein abcl polypeptides
Patent: WO 0078971-A 3 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                             2490 tttagaggaagcaaattccactggtgcccttggctgccgggaacgtggactagagtct 2549
                                                                                                                         Gaps
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0
                                                                                       Length 1643;
                                                                                               Pred. No. 3.9e-302;
                                                                                     16.7%; Score 541; DB 6;
100.0%; Pred. No. 3.9e-302
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
Patent: WO 0078972-A 3 28-DEC-2000;
                                                    403
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Sequence 3 from Patent W00078971.
                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
413 c 457 g 400
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Location/Qualifiers
         Decation/Qualifiers
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          CV THERAPEUTICS, INC.
                                                                                                        Matches 541; Conservative
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JOURNAL
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VERSION
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JOURNAL
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bockhett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 69570)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome, clone RP11-1N10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2430 ccaatccctccctccggctgaggaaactaacaaaggaaaaatugggaaagcagga 2489
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Homo sapiens clone RPll-1N10, LOW-PASS SEQUENCE SAMPLING.
AC021246
                                                                                                                                           ;
0
                                                                                                       Length 1643;
                                                                                                                                           0; Indels
                                                                                                         16.7%; Score 541; DB 6; L4
100.0%; Pred. No. 3.9e-302;
Live 0; Mismatches 0;
/organism="Homo sapiens"
/db_xref="taxon:9606"
413 c 457 g 403
                                   457 g
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                                                                                                                            Best Local Similarity 100.0
Matches 541; Conservative
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Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McEwan, F., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, E., McChark, A., McKernan, K., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Stojanovic, N., Severy, P., Spencer, B., Stange-Thomann, N., Tirlell, A., Vasslikev, R., Ylel, R., Vo, A., Wu, X., Myman, D., Ye, W.J., Direct Submission
                                                                                                                                                                                                                                Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 0. Jul 13, 2000 this sequence version replaced g1:6705871.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows vorlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This record contains 73 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Wortact: sequence_submissions@genome.wi.mit.edu
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contig of 851 bp in length
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10376: contig of 846 bp in length
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14241: contig of 861 bp in length
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13280: cont
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15196: cont
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16123: cont
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6540: con
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17072: c
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3880: gap of 100 bp 24733: contig of 853 bp in length 4833: gap of 100 bp 2570: gap of 100 bp 26521: contig of 851 bp in length 5770: gap of 100 bp 27576: contig of 855 bp in length 7676: gap of 100 bp 27576: contig of 855 bp in length 8653: contig of 856 bp in length 8653: contig of 866 bp in length 8653: contig of 866 bp in length 8653: contig of 860 bp in length 29492: contig of 860 bp in length
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100 bp
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f 864 bp in length
100 bp
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47599: contig of 856 bp in length
99: gap of 100 bp
48551: contig of 852 bp in length
51: gap of 100 bp
49485: contig of 834 bp in length
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2 40006; contig of 875 bp ir

7 4016; gap of 100 bp

4 41913; contig of 861 bp ir

8 41067; gap of 100 bp

8 41913; contig of 846 bp ir
                         18141: gap of 100 bp
19009: contig of 868 bp
19109: gap of 100 bp
19966: contig of 857 bp
17172: gap of 100 bp
18041: contig of 869 bp
18141: gap of 100 bp
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811 bp 1
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852 bp 1
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46643: contig of 819 bp
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43776: contig of
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49485; contig of
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47599: con+
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v: gap of
32368:
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31410: con
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33312: con
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36156: con
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37128: con
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ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                           AUTHORS
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ACCESSION
                                                             KEYWORDS
SOURCE
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                              52373 52472: gap of 100 bp
523473 53328: contig of 856 bp in length
53329 53428: gap of 100 bp
53429 54268: contig of 840 bp in length
54269 54368: gap of 100 bp
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contig of 868 bp in length
                                                                                                                                                                                                                                                                                         97: gap of 100 bp
57163: contig of 866 bp in length
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Pred. No. 7.2e-190;
0; Mismatches 1;
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66684: con
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Best Local Similarity 99.7%;
Matches 398; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center Clohe name: 1_M_10

Sequencing vector: M13, M7815; 100% of reads
Sequencing vector: M13, M7815; 100% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 14574 bases at least Q40
Consensus quality: 145749 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; sum-of-contigs
Quality coverage: 3.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L2510
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of 1707 bp in length
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contig of 1681 bp in length
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contig of 1270 bp in length
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contig of 1994 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 100 bp contig of 1531 bp in length
                                                                                                                     Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-1M10
Unpublished
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 AC012230.3 GI:7637254
HTG; HTGS_PHASE1; HTGS_DRAFT
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4516 5785: conf
5786 5885: gap of
5886 7879: conf
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7980 9686; cor
9687 9786; gap of
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1104 2634: cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2635 2734: gap of 2735 4415: cor
GI:7637254
                                                                                                           (bases 1 to 175064)
                                                          Homo sapiens
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100 bp

9786: gap

AC012230 175064 bp DNA linear HTG 22-APR-2000 Homo sapiens clone RPl1-1Ml0, WORKING DRAFT SEQUENCE, 39 unordered

pieces.

LOCUS

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7688 76988 39 001149 01330 bp in length 7688 82113; contig of 5125 bp in length 82114 82132; contig of 5125 bp in length 82214 88220; contig of 6007 bp in length 8821 8320; gap of 100 bp 8321 8320; gap of 100 bp 93500 93599; gap of 100 bp 93500 97901; contig of 4302 bp in length 9790 98001; app of 100 bp 9700 98001; app of 100 bp 9700 98001; app of 5015 bp in length 9790 98001; app of 5015 bp in length
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12253: contig of 2467 bp in length 53: gap of 100 bp
                      2254 12353: gap of 100 bp
2354 15228: contig of 2875 bp in length
                                                                                                     17201 17301: gap of 100 bp 17301 20131: contig of 2831 bp in length 20132 20231: gap of 100 bp 20232 22587: contig of 2356 bp in length
                                                               5229 15328: gap of 100 bp
5329 17200: contig of 1872 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                         45448: contig of 2513 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45548: gap of 100 bp
48116: contig of 2568 bp in length
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56592: contig of 3874 bp in length
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63661: contig of 3926 bp in length
63761: gap of 100 bp
68437: contig of 4676 bp in length
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76888: contig of 5330 bp in length
76989: gap of 100 bp
82113: contig of 5125 bp in length
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71458: contig of 2921 bp in length
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117408 124079: contig of 6672 bp in length
124080 124179: gap of 100 bp
124180 131281: contig of 7102 bp in length
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131382 138059: contig of 6678 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP11-1M10
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103117 109178: cont.
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52719 565
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155 aataggtaggagaagaagagagagagagatggagggtcagggagatctaattactctcta 214
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10.6%; Score 344; DB 2; I
Best Local Similarity 99.7%; Pred. No. 1.7e-187;
Matches 394; Conservative 0; Mismatches 1;
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22688 .25707
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68538. .71458
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71559. .76888
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/note="assembly\_fragment"

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3076 ggtaggagaaagagacgcaaacacaaaagtggaaaacaggtaagaggctctccagtgact 3135

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Submitted (23-AGG-2000) to the DDBJ/EWBL/GenBank databases. Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

Location/Qualifiers

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2 (bases 1 to 1750)

Isogai, T., and Otsuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                    1405 TGCCAAGGAGCTCAAAGGTTTCAACAAAGTTCACTTTCAGAAAACCCCTTTGAGGAAGAC 1346
                                                                                                 61 GGGCTGCGGCAGGGCAGGGCGGGGAGCTCCGCGCACAACAGAGCCGGTTCTCAGGGCGC 120
                                                                     335 agaatatacatctcccattttaaagatgaagaaacaggccgggcacaatggctaat 394
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oligo capping; fis (full insert sequence).
Homo sapiens Mammary gland cDNA to mRNA, clone_lib:MAMMAA
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AK022254
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/note="cloning vector: pME18SFL3"
489 c 586 q 384 t
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                                                                                                                                                                      395 gcctgtaatcccagcactttggggaggctgaggcca 429
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/db_xref="taxon:9606"
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Matches 336; Conservative
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/product="ATP binding cassette transporter 1"
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/xranslation="MACWPQLRLHWWGIICNANNPCFRYPTPGEAPGVVGNFNKS"
198 c 190 g 156 t others
                                                                                                                                                                                                                                                                     oy/ bp mRNA linear PRI 11-MAY-2000 Homo sapiens ATP binding cassette transporter 1 (ABCA1) mRNA, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
Analysis of hABC1 gene 5' end: additional peptide sequence,
promoter region, and four polymorphisms
Biochem. Biophys. Res. Commun. 271 (2000) In press
2 (bases 1 to 697)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Direct Submission
3136 tacttgggcgttattgttttgtttcgaggccaaggaggcttcgggaagtgctcggtttcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.4%; Score 303; DB 9; Length 697;
100.0%; Pred. No. 6.1e-164;
tive 0; Mismatches 0; Indels
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                                                                                                                                                             301 GGGACTTTGATCCGGAGCCCCACATCCCCACCTT 336
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/db_xref="taxon:9606"
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1. .>697
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/note="ABC1"
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4816: co
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldakin, J., Barna, N., Beckerly, R., Bedak, F., Lanton, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Choepel, T., Galagan, J., Rerietta, P., FitzHugh, W., Porrest, C., Gage, D., Galagan, J., Rarta, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Manquis, N., McBwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Plerre, C., Connor, T., O'Connor, T., O'Lora, T., M., Peterson, K., Plerre, N., Pillara, V., Raymond, C., Rilley, R., Rothman, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wuyman, D., Ye, W.J., Zimmer, A. and Zody, M., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Wassiliev, H., Viel, R., Vo, A., Wuyman, D., Ye, W.J., Direct, Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90698)
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caacagagccggttctcagggcgctttgctccttgtttttccccggttctgttttctcc
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                                        241 CCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAGAGACGCAAACACAAAAAGTGGAAAA 300
                                                                                                      ACO21345 90698 bp DNA linear HTG 1
Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING.
ACO21345
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
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26 45425; gap of 100 bp 100 bp 100 44305; contig of 880 bp in length 100 bp 100 44302; contig of 891 bp in length 100 bp 10 51309: gap of 100 bp 10 5221: contig of 912 bp in length 100 sp 100 s 25 5724; gap of 100 bp 36 34535: gap of 100 bp 36 55433: contig of 898 bp in length 37 3533: gap of 100 bp 37 3540: contig of 907 bp in length 11 36540: gap of 100 bp 11 37422: contig of 882 bp in length 23 37522: gap of 100 bp 65115: gap of 100 bp 65975: contig of 860 bp in length 66075: gap of 100 bp 67054: gap of 100 bp 100 bp 67054: gap of 100 bp 67947: contig of 893 bp in length 67947: contig of 893 bp in length 61167: gap of 100 bp 62051: contig of 884 bp in length 62151: gap of 100 bp 63022: contig of 871 bp in length 63122: gap of 100 bp 64026: contig of 904 bp in length 69034: gap of 100 bp 69910: contig of 876 bp in length 68934: contig of 887 bp in length p of 100 bp contig of 889 bp in length 38502: gap of 100 bp 39380: contig of 878 bp in length 39480: gap of 100 bp 440407: contig of 927 bp in length 40507: gap of 100 bp 41405: contig of 898 bp in length 505: gap of 100 bp 42399; contig of 894 bp in length 199; gap of 100 bp 43357; contig of 858 bp in length 57: gap of 100 bp 44356: contig of 899 bp in length 56: gap of 100 bp 45325: contig of 869 bp in length 38402: contig of 880 bp in length 02: gap of 100 bp 34435: contig of 888 bp in length 64126: gap of 65015: cont 43457: gap of 16406 473( 17303 47402: 44456: 42499 41505 67948 68048 68935 69035 60059 60159 59176

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Schmitz, G. and Bodzioch, M.
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Parent: WO 0170810-A 3 27-SEP-2001;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Dene.
Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.
Regulatory nucleic acid sequences of the abol gene
Patent: WO 0183746-A 4 08-NOV-2001;
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AK024328
AK024328.1 GT:10436685
AK024328.1 GT:10436685
Homo capping; fis (full insert sequence).
Homo saplens placenta cDNA to mRNA, clone_lib:PLACE1
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/db_xref="taxon:9606"
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Direct Submission
Submitted (22-Aug-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; CDNA full insert
sequencing: Research Association for Biotechnology; CDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
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SYPPYEQHECHFPNKAMPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIV
ARLFSDARRLLLYSQKDTSMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYH
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KELAAAERTULSNUDILKPILMDVACDDIAHGQLTVPRSAAVAATGDAKPNIMGRET
LLSTCASVPRVVEFHERHILEHFSFCVCVSVSLFPAKGIVSFSMASFRIWVLWRAVFWQ
HGESMAVWEGQLGGLNIAFEYFTSIDVG"
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1 (bases 1 to 9634)
Denefie, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H., Remaley, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and
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/clone_lib="PLACE1"
/note="cloning vector: pME18SFL3"
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AX127831
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/db_xref="GI:10436686"
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/clone="PLACE1002437"
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1 (bases 1 to 9854)

Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C., Naudin,L., Lemoline,C., Duverger,N., Jaye,M., searfoss Iii,G.H., Remaley,A., Brewer,H.B. and Dean,M.

Nucleics acids of the human abcl gene and their therapeutic and
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Patent: EP 1096012-A 70 02-MAY-2001;
    diagnostic application
Patent: WO 0130848-A 70 03-MAY-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
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/db_xref="taxon:9606"
2219 c 2334 g 2635
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/db_xref="taxon:9606"
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1 (bases 1 to 10442)
Lawn, R.M., Wade, D. and Garvin, M.
Eawn, R.M., Wade, D. and Garvin, M.
Pegulation with binding cassette transporter protein abcl
Patent: WO 0078972-A 1 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10442)
Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
Arb binding cassette transporter protein abc1 polypeptides
Patent: WO 0078971-A 1 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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/db_xref="taxon:9606"
a 2297 c 2408 g 283:
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/db_xref="taxon:9606"
1 2297 c 2408 g 283:
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AX060892
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181 ACGCAAACACAAAAGTGGAAAACAG 205
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Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA, AF285167 AF285167.1 GI:9755158
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ARLFSDARRLLLYSQKDTSMKDMRKYLRTLQQIKKSSSNLKLQDFLYDNETFSGFLYH
NLSLPKSTVDKMLRADYILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP
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SYSDKRQFWPTTNTNNSSSSSTGVIZVACVSRIVCOFPBEGGGEKKKSLMWYEDNNYKALF
GGNGTEEDAETFYDNSTTPYCNDLAKNLESSPLSRIJWKALKPLLVGKILYTPDTPAT
RQVMAEVNKTFQELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMLLDSRDNDHFWE
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KLEPIATEVWLINKSMELLDERKFWAGIVFTGITPGSIELPHHVKYKIRMDIDNVERT
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Lawn,R.M., Wade,D.P., Garvin,M.R., Wang,X., Schwartz,K.,
Lawn,R.J.G., Sellhamer,J.J., Vaughan,A.M. and Oram,J.F.
Direct Submission (106-JUL-2000) Discovery Research, CV Therapeutics Inc.,
3172 Porter Drive, Palo Alto, CA 94304, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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          Length 10442;
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/protein_id="AaF98175.1"
/db_xref="GI:9755159"
                                                0; Indels
  6.1%; Score 197; DB 6;
100.0%; Pred. No. 3e-102;
vative 0; Mismatches 0;
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/db_xref="taxon:9606"
/chromosome="9"
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1. .10442
/gene="ABCA1"
291. .7076
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Best Local Similarity 100.0
Matches 197; Conservative
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BQGIGVQWDNLFESPVEEDGFNLTTSISMMLPDTFLYGVWTWYIEAVFPGQYGIPRPW
YFPCTKSYWFGEESDEKSHPGSNQKRMSEICMEEBPTHLKLGVSIQNLVKVYRDGMKV
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LTGDTTVTRGDAFLNKNSILSNIHEVHONMGYCPQFDAITELLTGREHVEFFALLRGV
PEKEVGKVGEWAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTG
FSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFVFLSVFAVVTILQCFLISTLF
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FSILSQSKKRLHIEDYSVSQTTLDQVFVNFAKDQSDDHLKDLSLHKNQTVVDVAVLT
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I bases 1 to 10474)

Lawn, R.M., Wade, D. and Garyin, M.

Regulation with binding cassette transporter protein abc1

Patent: WO 0078972-A 7 28-DEC-2000;

CV THERAPEUTICS, INC. (US)

Location/Qualifiers

1. .10474
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Sequence 7 from Patent WO0078972.
AX060719
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Matches 197; Conservative
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Lawn, R.M., Wade, D. and Garvin, M.
Lawn, R.M., Wade, D. and Garvin, M.
Patent: WO 0078972-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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5.8%; Score 188; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 5e-97;
Matches 188; Conservative 0; Mismatches 0; Indels 0
                                                                                   Length 10474;
                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                5.8%; Score 188; DB 6; Length 104
100.0%; Pred. No. 5e-97;
tive 0; Mismatches 0; Indels
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2305 c 2416 g 2843
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Sequence 9 from Patent W00078972.
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       PAT 22-JAN-2001
                                                                                                        Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 10474)

Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.

Patp binding caseste transporter protein abcl polypeptides

Patent: WO 0078971-A 7 28-DEC-2000;

CV THERAPEUTICS, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10474)
Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abcl polypeptides
Patent: WO 0078971-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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Sequence 7 from Patent W00078971.
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/db_xref="taxon:9606"
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Location/Qualifiers
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will be sequenced to completion. In the event that
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Direct Submission

L. Submitted (16-Jan-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                           HTG 13-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90698)
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                                                                       cgcaccaacagagccggttctcagggcgctttgctccttgttttttccccggttctgttt 3046
                                                                                                                                                                3047 teteceetteteeggaaggettgteaaggggtaggagaaagagagaegeaaacaeaaagtg 3106
                                                                                               102 CGCACCAACAGAGCCGGTTCTCAGGCCCTTTGCTCCTTGTTTTTTCCCCCGGTTCTTT 161
    162 TCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAAAAGAGACACAAACACAAAAGGG 221
                                                                                                                                                                                                                                                                                                                                                                                                        ACU21345 90698 bp DNA linear HTG 1.
Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING.
AC021345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L4483
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REFERENCE

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COMMENT

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15662: contig of 100 bp 15662: contig of 878 bp in length 15762: gap of 100 bp 1677: contig of 915 bp in length 16777: gap of 100 bp 1777: gap of 100 bp
is updated, the accession number will
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32452: contig of 899 bp in length
                                         contig of 910 bp in length
                                                                                                                                                 of 100 bp contig of 878 bp in length
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Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
Brewer,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 6 08-NOV-2001;
Aventis Pharma S.A. (FR)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Score 152; DB 2; Lv
Pred. No. 5.1e-76;
0; Mismatches 2;
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Best Local Similarity 100.0%; Pred. No. 5.4e-56;
Matches 117; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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Sequence 6 from Patent WO0183746.
AX351034
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Sequence 69 from Patent WO0130848.
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AX127830.1 GI:14134477
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1 (bases 1 to 446)

Denefielp., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Jaye,M., searfoss Ili,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
Nucleics acids of the human abcl gene and their therapeutic and
diagnostic application
Patent: EP 1096012-A 3 02-MAY-2001;
Aventis Pharma S.A. (FR)

Location/Qualifiers
1 (bases 1 to 446)
Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
Abent: WO 0130848-A. 3 03-MAY-2001;
Aventis Pharma S.A. (FR)
Loction/Qualifiers
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/db_xref="taxon:32630"
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                                                                                                                                                                    /organism="synthetic construct"
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9741)
Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Rwudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and diagnostic application
Patent: W. 0130848-A 69, 03-MAX-2001;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 69 from Patent EP1096012.
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/organism="Homo sapiens"
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VERSION

KEYWORDS

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ORGANISM

REFERENCE AUTHORS BASE COUNT

ORIGIN

JOURNAL

TITLE

FEATURES

Matches

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Submitted (13-FEB-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 1 to 126295)

B irran, B. Fasman, K. Lintcon, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Colangelo, M., Collins, S., Collymore, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Castle, A., Cerny, J., Colangelo, M., Porner, K., Donelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Garalgery, K., Grant, G., Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdot, A., Heaford, A., Herena, L., Horton, L., Howland, J.C., Jacotot, L., Molla, M., Morris, W., McGurk, A., McGernan, R., McHrim, J., Molla, M., Morris, W., McGurk, A., McGernan, R., Mahdrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Stange-Thomann, M., Stilwell, J., Stojanovic, N., Yorruella-Miller, I., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W. J., Zhao, J. and Zody, M.

Submitted (Oz-SEP-1998) Whitehead Institute/MIT Center for Genome Search, 320 Charles Street, Cambridge, MA 02141, USA on Sep 2, 1998 this sequence version replaced gi:3451370.

All repears were identified using RepeatMasker: Smit, A.F.A. & Locator/Obalifiers

Location/Quallifiers

Location/Quallifiers
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complement(2. .193)
/rpt_family="AluSx"
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/rpt_family="MER5B"
complement(2647. .2954)
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complement(6403. .6675)
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6782. .6950
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complement(8759...9456)
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/rpt_family="MER5B"
3758. 4544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .8597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7379. .7734)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .7840)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(714. .1012)
/rpt_family="Alusc"
1140. .1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="Tigger1"
complement(8604. .8741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(235. .410)
/rpt_family="MER5A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="Tigger1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .640)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="L2"
4743. 4873
/rpt_family="FLAM_C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="Tiggerl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="(GGGA)n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="HRPC843B9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
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                                                                                                                                               AUTHORS
                                                                                                          REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
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S Birren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P.,
Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R.,
Lander, E., Allen, N., Baker, J., Castle, A., Cerny, J., Cooke, P.,
Boutwell, C., Byrne, S., Cantu, C., Castle, A., Cerny, J., Cooke, P.,
Daly, M.J., Depayre, E., Devon, K., Dewar, K., Donelan, L., DuRette, B.,
Etemadi, S., Ferreira, P., Forrest, C., Funke, R., Gage, D., Gardyna, S.,
Gensheimer, S., Gerajgery, K., Gilmartin, T., Garay, D., Hagos, B.,
Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Linton, L.,
MacKenzie, J., Marquis, N., McEwan, P., McGurk, A., Meldrim, J.,
Molla, M., Morris, W., Morrow, J., Nachman, A., Naylor, J., O'Connor, T.,
Pavlin, B., Peterson, K., Ranganath, S., Riley, R., Roberts, D.,
Rollins, G., Rossello, R., Roy, A., Shyam, R., Soohoo, S.,
Stange-Thomann, N., Stilwell, J., Stone, C., Strickland, C., Sydney, K.,
Tang, L., Vassillev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y.,
Ye, W.J., Zamtseva, I., Zhao, J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRI 02-SEP-1998
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3023 cttgttttttccccggttctgttttctccccttctccggaaggcttgtcaaggggtagga 3082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 17, clone HRPC843B9, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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100.0%; Pred. No. 2.9e-41;
tive 0; Mismatches 0; Indels
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone HRPC843B9
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                                                                                                                                                                                                                                                                 AX351038 9741 bp
Sequence 10 from Patent WO0183746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
2180 c 2290 g 2620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GAAAGAGGCGAAACACAAAAGTGGAAAACAG 92
                                61 GAAAGAGGCAAACACAAAAGTGGAAAACAG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126295 bp
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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SOURCE ORGANISM

KEYWORDS

VERSION

JOURNAL REFERENCE AUTHORS

TITLE

REFERENCE AUTHORS

TITLE

DEFINITION

LOCUS

ACCESSION

RESULT 31

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/rpt_family="LiMBC"
complement(1555)
.rpt_family="LiMBC"
complement(1552)
.complement(1562)
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/rpt_family="(CAAAA)n"
complement(20169. .20451)
/rpt_family="Alusx"
complement(20456. .20765)
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complement(13066. .13222)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="MIR"
complement(19656. .19771)
/rpt_family="MER20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(18474. 18774)
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/rpt_family="L2"
complement(25816, .25978)
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/rpt_family="MLT1G"
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22291. .22526
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complement(9467. .9759)
/rpt_family="AluSx"
complement(9820. .10276)
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10754. .11095
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13545. 13769
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14208. 14364
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complement(20145. ...
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23606. .23899
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ACU21850 206966 bp DNA linear PRI 09-MAY-2001
Homo saplens BAC clone RP11-389E17 from 4, complete sequence.
ACU21850
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Waterston, R.H.
Direct Submission
Submitted (20-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Materston, R.H.
Materston, R.H.
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Submitted (16-FEB-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 206966)
Waterston, R.
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Sulston, J. E. and Waterston, R. Toward a complete human genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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Kang, K., Maupin, R. and Ureta, M.
The sequence of Homo sapiens BAC clone RP11-389E17
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.0%; Score 65; DB 9; L
Best Local Similarity 100.0%; Pred. No. 1.8e-25;
Matches 65; Conservative 0; Mismatches 0;
complement(28773, .29080)
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36517. 36689
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AUTHORS

'rpt\_family="AT\_rich"

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repeat_region
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WETCHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-62B4. Actual start of this clone is at base position 1 of RP11-389E17; actual end is at base position 206966 of RP11-389E17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mapping information for this clone was provided by Dr. John D. Werberson. Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
Direct Submission
Submitted (09-MAY-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 16, 2001 this sequence version replaced gi:11761497.
                                                                                                                                                                                                                                                                                                                                                                                    NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                     Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                         Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                Center project name: H_NH0389E17
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/db_xref="taxon:9606"
/chromosome="4"
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531. .2753
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2987. .3022
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3223. .3260
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1779. 1908
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1930. 1950
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1088. .1319
                                                                                                                                                                                    Center code: WUGSC
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12950. .13462
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Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abcal)
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Qlu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submitted (14-JUL-2000) Genome Science Department, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Qlu,Y., Caveller, Chiu,S., Yang,X., Rubin,E. and Cheng,J.F.
Human and mouse abcal comparative sequencing and transgenesis
studies revealing novel regulatory sequences
Genomics 73 (1), 66-76 (2001)
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1010(87184 . 87402.103551 .103699.115064 .115187,

119217 .119358.120364 .120482,133479. 133400,

135582 .135758.147083 .147175,149791 .150031,

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160617 .160888 .167790 .161994,163076 .163189,

164646 .164817,165738 .165869,167171 .167313,
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tive 0; Mismatches 0; Indels
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35013. 35078
/rpt_family="AT_rich"
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/rpt_family="(CA)n"
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40826. .41020
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34635. .34825
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YVDDIFLKRWSKSMPLFMTLAMIYSVAVIIKSIVYREARLKETMRINGLDNGTLWFS
WFVSSLIPLLVSAGLLVVILKLGNLLPYSDPSVYFYSLSVFREARWTILQCFLISTLERR
ANLAAACGIIYTLXLPYVLCVAWQDYVGFSIKIFASLLSPVARFGFGCESFFLIFERG
GIGVOMDNLFESPVEEDGFNLTTANSMALFDTFLYGVMTWYITANFFGCGEFFLFEED
GCTKSYWFGEEIDEKSHPGSSOKGVSEICMEEPFTHRAGSTGNLYRTGGMRVAV
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LGVCPQHNVLEDMLTYEEHINFYARLKGLSEKHVKABMEQMALDVGLPPSKLKSKTSO
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NNTEEDVDFFFYDNSTYPYCNDLMKNLESSPLGSRIWKALKPLLVGKILYTPDFPATRQ
NNATEDVOFFFYDNSTYPYCNDLMKNLESSPLGSRIWKALKPLLVGKILYTPDFPATRQ
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EDGLDWTAQDIMAFLANDFEDVOSPNGSYPKREAFNESTNQALQFISRFMCVNLNKL
EPIPTEVRLINKSMELLDERKFWAGIVFTGITPDGVELDHHVKYKIRMDIDNVERTNK
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MDAEDTLIGGRATALISHRKLCCVGSSLFLKNOLGTGYYLTLVKKOVESSLSCRRSST
VSCLKKEDSVSQSSDAGLGSDHESDTLTINSALSLIRKHYSEARLVEDIGHELTV
VLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEEGGVDAFTSDG
KLTQQQFVALLWRKLIARRSRRGTSDAVDNDSDIDPESRFIDLLSGMCKGSYQLKGW
KLTQQQFVALLWRKLIARRSRRGTSQULPAVFVCTALVFSLIVPPFGKYPSLELD
PWMYNBQYTFVSNDAPEDMGTQELLNALIKNENDRGSGTRCMEGNPIPDTPCLLAGEEDWTI
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SLPRSTVDSLLQANVGLQKVFLQGYQLHLASLCNGSKLEEIIQLGDAEVSALCGLPRK
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LQMUTGRNISDYLWKTYQIIAKSLKNKIWVWEFRYGGFSLGVSNSQALPPSHFWNDA
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RANLQKGENPSQYGIIAFNHPLNLTKQQLSFVALMTTSVDVLVSICVIFAMSFVPRASF
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SSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVAFFVL
ELFTNNKLNDINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW
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GGGQNDILEIKELTKIYRRRRPAVDRICIGIPPGECFGLLGVNGACKSTTFKMLTGD
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GYTIVVRIAGSNPDLKPVQEFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILS
QSKKRLHIEDYSVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQD
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkly, L., Boukhgalter, Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Calagelo, M., Callins, S., Callymore, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grahm, L., Garnd-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karlass, A., Kells, C., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Lethie, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Micol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Retta, R., Reback, M., Riley, R., Santos, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thoman, N., Stohupback, R., Seaman, S., Strinss, N., Suhramanian & Arlaman, A., Allamanian & Allaman, A., Allaman, A., Allamas, A., Santos, A., Santos, S., Schupback, R., Seaman, S., Strinss, N., Suhramanian & Allaman, M., Stohupback, R., Seaman, S., Strinss, N., Suhramanian & Allaman, M., Stohupack, R., Seaman, S., Strinss, N., Suhramanian, M., Stohupack, R., Seaman, S., Strinss, N., Suhramanian, M., Stanger, M., Santos, M., S
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Homo sapiens chromosome 11 clone CTD-2028015 map 11, LOW-PASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 57662)
                                                                                                                                                                                                                                                                                                                                                 Straus, N. Subramann, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Center: Whitehead Institute/ MIT Center for Genome Research
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                         255 others
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4.1e-23;
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                                                                                                                                                                                             Query Match
1.9%; Score 61; DB
Best Local Similarity 100.0%; Pred. No. 4.1
Matches 61; Conservative 0; Mismatches
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Center project name: L24518
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\* NOTE: This record contains 73 individual

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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2486; gap of 100 bp 13187; contig of 701 bp in length 13988; contig of 701 bp in length 4088; gap of 100 bp 14795; contig of 707 bp in length 495; gap of 100 bp 1532; contig of 637 bp in length 15532; contig of 637 bp in length 16347; contig of 715 bp in length
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                                                                                                                                                           718 817: gap of 100 bp
818 1525: contig of 708 bp in length
1526 1625: gap of 100 bp
1626 2365: gap of 100 bp
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13927: contig of 718 bp in length
1466: contig of 719 bp
1746: gap of
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139375: contig of 688 bp in length

75: gap of 100 bp

40179: contig of 704 bp in length

179: gap of 100 bp

40986: contig of 707 bp in length
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33009: contig of 637 bp in length
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together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                              HS931E15
Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSS, GSSs and genomic marker DXS8098, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/HGP/ChrX
931E15 is from the library RPCI5 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see http://Dacpac.med.buffalo.edu/ VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone 931E15.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-SEP-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 18, 1998 this sequence version replaced gi:3550203.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neighbouring submissions.
The true left end of 424J12 (282213) is at 37431.
The true right end of 5052 (282213) is at 37431.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                Oy 1187 ctgcccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 1244
Db 39017 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGGGCCCAGC 38960
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702. .100?
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/note="Alusp repeat: matches 1. .302 of consensus"
1010. .1178
                                                                                                                           ö
                                                            Length 57662;
                                                                                                                           0; Indels
54444: contig of 679 bp in length
                                                            th 1.8%; Score 58; DB 2; L Similarity 100.0%; Pred. No. 1.9e-21; 58; Conservative 0; Mismatches 0;
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HTG; DXS8098.
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Direct Submission
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                                                                  Query Match
Best Local Similarity
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JOURNAL
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KEYWORDS
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/note="FRAM repeat: matches 5. .166 of consensus"

Anote="AluJb repeat: matches 300. .1 of consensus" (note="AluJb repeat: matches 2 .302 of consensus" 5170 .1547 .1504 (note="AluJb repeat: matches 3627 .3966 of consensus" 5170 .1547 .1 repeat: matches 1 .302 of consensus" 5144 .5948 .3643 repeat: matches 1 .303 of consensus" 5644 .5948 repeat: matches 1 .303 of consensus" 5644 .5948 repeat: matches 1 .303 of consensus" 5644 .5948 repeat: matches 1 .303 of consensus" 6156 .6629 .6879 .0879 .139) .4731 of consensus" 6156 .6829 .8879 .4339 of consensus" 6156 .6809 .1399 .7038 .762 /note="Alusx repeat: matches 4. .302 of consensus" 12439. .12940
/note="LiMes repeat: matches 166. .685 of consensus" complement(13266. .13588)
/note="match: STS L40936" /note="AluSx repeat: matches 2. .302 of consensus" 13958. .14050 /note="AluSx repeat: matches 1. .93 of consensus" 14055. .14323 /note="AluSx repeat: matches 60. .301 of consensus" 14514. .14836 /note="AluJb repeat: matches 13. .302 of consensus" 12126. 15428 /note="AluSx repeat: matches 1. .302 of consensus" 15626. .15730 /note="AluSx repeat: matches 1. .300 of consensus" 2767. .3067 / ...3067 / ...atches 1. .302 of consensus" complement(4220. .4537) / ...atches 300. .1 of consensus" /note="AluJb repeat: matches 300. .1 of consensus" complement(1365, .1664) /note="match: STS G05254" repeat\_region misc\_feature misc\_feature

74100: ..44231
7.00te="32 copies 2 mer aa 80% conserved"
24520. .24884
7.00te="11PA5 repeat: matches 517. .890 of consensus"
7.00te="11PA5 repeat: matches 157. .890 of consensus"
7.00te="MER20 repeat: matches 155. .1 of consensus"
7.00te="32 copies 2 mer tt 83% conserved"
7.00te="32 copies 2 matches 195. .5 of consensus"
7.00te="Aluxb repeat: matches 3 .300 of consensus"
7.10f5. .27462
7.00te="Aluxb repeat: matches 2 .302 of consensus"
7.00te="Aluxb repeat: matches 1 .29% of consensus"
7.00te="Aluxb repeat: matches 1 .29% of consensus"
7.00te="Aluxb repeat: matches 2 .302 of consensus"
7.00te="Aluxb repeat: matches 3 .206 of consensus" 19901. 20160
/note="Alux repeat: matches 39. 298 of consensus"
complement(20716. 20882)
/note="Malux repeat: matches 260. 69 of consensus"
complement(20824. 21385)
/note="match: GSSs B94184 AQ010265"
21550. 23628
/note="putative CpG island"
complement(22542. 22581)
/note="MIR2 repeat: matches 134. .95 of consensus"
complement(23094. 24185)
/note="Systa repeat: matches 1101. .1 of consensus"
24186 24231 /note="AluJb repeat: matches 196. .300 of consensus" 16118. .16420 /note="WERAB repeat: matches 11. .148 of consensus" 32041. .32319 /note="Alux repeat: matches 1. .287 of consensus" complement(32381. .3359) /note="MLT2\_internal repeat: matches 4572. .3316 of complement(30513. .30706) /note="MLT2\_internal repeat: matches 4754. .4572 of complement(28817. .29089)
/note="Alusx repeat: matches 298. .2 of consensus"
29122. .29252
/note="L1 repeat: matches 3151. .3280 of consensus"
complement(29957. .30200)
/note="MLT2\_internal repeat: matches 5375. .5124 of /note="FLAM\_A repeat: matches 117. .6 of consensus" complement(17160. .17224)
/note="MIR repeat: matches 149. .84 of consensus" 30728. .31025 .0.0tc="Alusx repeat: matches 1. .299 of consensus" 31059. .31356 .7.note="Alusy repeat: matches 1. .296 of consensus" 31359. .31505 33603. .33906 /note="AluJo repeat: matches 1. .302 of consensus" 4020. .34321 /note="AluJb repeat: matches 1. .301 of consensus" complement(34388. .34933) /#8120. .18226 /note="match: STS L24586" complement(18124. .18827) /note="match: GSS B16653 B14990" complement(19378. .19676) /note="alusp repeat: matches 303. .2 of consensus" /note="AluJb repeat: matches 1. .290 of consensus" complement(16828. .16935) consensus consensus consensus repeat\_region epeat\_region repeat\_region misc\_feature misc\_feature misc\_feature misc\_feature

Query Match 1.8%; Score 58; DB 9; Length 81874;
Best Local Similarity 100.0%; Pred. No. 2e-21;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gap

0;

HSDJ247C2/c

DEFINITION

ACCESSION

KEYWORDS

VERSION

ORGANISM

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

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.26158)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, Cabonitted (02-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Sep 27, 2000 this sequence version replaced gi:6006528.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; T:, TREMBL; WP:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep IMPORTANT: This sequence is not the entire insert of clone RP1-247C2 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP1-247C2 is at 1 in this sequence. The true left end of clone RP1-879J8 is at 98261 in this sequence. The true right end of clone RP5-8866 is at 4651 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RPI-247C2 is from the flurther details see
                                                                                                                                                                     HSDJ247C2 98360 bp DNA linear PRI 03-AUG-2001 Human DNA sequence from clone RP1-247C2 on chromosome 11p13 Contains STSs and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="LlPA11 repeat: matches 2154. .2191 of consensus"
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/note="L1PA11 repeat: matches 2180. .2215 of consensus"
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/note="L1DA01 repeat: matches 3216. 6162 of consensus'
10697. 11906
/note="L1MEc repeat: matches 2142. 1979 of consensus"
Db 39890 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC 39833
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'note="L1PA11 repeat: matches 2215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="match: STS: Em:HS198YB10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(627.
                                                                                                                                                                                                                                                                                            AL049713.20 GI:10334639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 98360)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wallis, J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
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source

FEATURES

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Complement(8407. 4564)

Chote="match: GSS: Em:AJ247033"
53815. 53904

/note="Charlie2 repeat: matches 3272. 3370 of consensus"
54009. 54335

Anote="Charlie2 repeat: matches 2888. 3117 of consensus"
56236. 57009

/note="L1PA2 repeat: matches 1. 776 of consensus"
57005. 62248

/note="L1PA2 repeat: matches 900. 6144 of consensus"
63508. 63508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42053. .42372
/note="Charliela repeat: matches 778. .1137 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40351. .40840
/note="Charliela repeat: matches 277. .769 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38956. .39215
/note="Charliela repeat: matches 28. .281 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match: GSS: Bm:A2393320"
26106. .26561
/note="match: GSS: Em:A2393320"
29550. .29536
/note="LIMA8_repeat: matches 6175. .6268 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  // Note="Light are peat: matches 5743. .6147 of consensus" 37497. .37542  
// Note="23 copies 2 mer tg 100% conserved"  
// Note="match: STS: Em:445608"  
// Note="match: STS: Em:AU048503"  
// Note="match: STS: Em:AU048503"  
// Note="match: STS: Em:AU046429"  
// Note="match: STS: Em:AU046429"
/note="L1MEc repeat: matches 1978. .2279 of consensus"
                                                                                                                                                                                                                                                                                                                                                  17380. 17654
/note="MLT1A2 repeat: matches 92. .374 of consensus"
complement(17710. .18372)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="17 copies 2 mer aa 82% conserved"
63586. .63668
/note="LIMD repeat: matches 738. .819 of consensus"
                                                                                                                                                                                                                                                                                                                          /note="MLT1A2 repeat: matches 1. .92 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .98 of consensus"
                                                                                                                                                                                                    ρλ
                                                                                               /note="LTR2 repeat: matches 1. .449 of consensus" complement(14642. .15322)
                                                                                                  complement(14642. 15322)
/note="match: GSS: Em:B04935"
15910. 15911
/note="Single clone region. Assembly confirmed lestriction digest data."
15930. 15955
/note="13 copies 2 mer tg 92% conserved"
                    13794. .13857
/note="32 copies 2 mer cc 68% conserved"
14618. .15078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="31 copies 2 mer gt 91% conserved" 38956. .39215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33434. .33473
/note="LTR29 repeat: matches 56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(17710. .18372)
/note="match: GSS: Em:AQ485260"
18444. .18750
complement GSS: Em:AQ545989"
complement 20477. .21170)
/note="match: GSS: Em:AQ488664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /hote="match: GSS: Em:A2398168"
18685. 38746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(20761. .21177)
/note="match: GSS: Em:AQ669825"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: GSS: Em:AQ505438"
25991. .26104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44071. .44491
/note="match: GSS: Em:AQ112832"
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2 [bases I to 145178]

8 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chasaro, B., Cooke, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, Y., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Faro, S., Fareira, P., FitzBiugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lancque, K., Lanczares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McCann, C., Marquis, N., Matthews, C., McCarthy, M., McCwan, P., McKernan, K., Marquis, N., Matthews, C., McCarthy, M., McCwan, P., McKernan, R., Meldrim, J., Weneus, L., Mihova, T., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, S., Severy, P., Spencer, B., Stange-Thoman, N., Stolapov, R., Poman, S., Strauss, N., Subramanian, A., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, N., Yew, Willow, Y., Wyman, D., Ye, W.J., Young, G., Viel, R., Vo, A., Wilson, B., Wyman, D., Ye, W.J., Young, G., Viel, R., Vol, A., Wilson, B., Wyman, D., Ye, W.J., Young, G., Viel, R., Vol, A., Wilson, B., Wyman, D., Ye, W.J., Young, G.,
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                                                                                                                                                                                                  complement(76094..76635)

/note="match: GSS: Em:AQ277578"

ure complement(76184..76636)

ure complement(76184..76636)

ure complement(76460..76638)

/note="match: GSS: Em:AQ81253"

rooplement(88581..89052)

/note="match: GSS: Em:AQ10871"

re complement(88581..89052)

/note="match: GSS: Em:AQ201907"

re fnote="match: GSS: Em:AQ543464"

ion 91625..91990

/note="THELC repeat: matches 1..371 of consensus"

lon 92079..9237

/note="LibA7 repeat: matches 5949..6125 of consensus"

/note="LibA7 repeat: matches 5949..6125 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 145178)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 11, clone RP11-4809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome 11 clone RP11-4809 map 11, WORKING DRAFT SEQUENCE, 3 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD 18635 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC 18578
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63917. .64021
/note="LIMD repeat: matches 984. .1089 of consensus"
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0
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Pred. No. 2e-21;
0; Mismatches 0; Indels (
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HTG; HTGS_PHASE2; HTGS_FULLTOP
                                                    complement(64074. 64543)
/note="match: GSS: Em:AQ885350"
complement(66096. 66577)
/note="match: GSS: Em:AQ611651"
69990. .70342
/note="match: STS: Em:G21603"
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Best Local Similarity 100.(
Matches 58; Conservative
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AUTHORS
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KEYWORDS
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Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 13, 2002 this sequence version replaced gi:18308666.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: 48_0_9

Center clone name: 48_0_9

Sequencing vector: Plasmid; n/a; 100% of reads
Cenmistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 144836 bases at least Q40

Consensus quality: 144952 bases at least Q20

Insert size: 141000; agarose-fp

Insert size: 144078; sum-of-contigs
Quality coverage: 18.7 in Q20 bases; sum-of-contigs
Quality coverage: 18.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 68019: contig of 68019 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                          Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 others
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140461 140560: gap of 100 bp
140561 145178: contig of 4618 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-11 Human Male BAC"
1. .68019
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector_side:right"
46626 a 28900 c 28355 g 41097 t
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68120. .140460
/note="assembly_fragment"
140561. .145178
/note="assembly_fragment
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/db_xref="taxon:9606"
/chromosome="11"
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1. .145178
                                                                                                                                                                                                                                      Genome Center
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Homo sapiens
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AC015495
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                                                       AC015494 146312 bp DNA linear HTG 26-MAY-2001
Homo sapiens clone RP11-21E12, WORKING DRAFT SEQUENCE, 12 unordered
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 146312)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-21E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAY 26, 2001 this sequence version replaced gi:13443216.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Center: Whitehead Institute/ MIT Center for Genome Research
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Sequencing vector: mais m77815; 3% of reads
Sequencing vector: plasmid; n/a; 97% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 14250 bases at least Q40
Consensus quality: 144014 bases at least Q30
Consensus quality: 14450 bases at least Q20
Insert size: 145212; sum-of-contigs
Quality coverage: 9.4 in Q20 bases; agarose-fp
Quality coverage: 8.3 in Q20 bases; agarose-fp
Quality coverage: 8.3 in Q20 bases; are represented as a is not known and their order in this sequence record is
* runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1833 2945; contig of 1113 bp in length
2946 3045; gap of 100 bp
3046 1115; contig of 1071 bp in length
4117 4216; gap of 100 bp
4217 5757; contig of 1541 bp in length
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                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                                                             AC015494
AC015494.6 GI:14209771
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RESULT 43
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of 100 bp
contig of 1688 bp in length
                                                                                of 100 bp contig of 3882 bp in length
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/clone=lib="RPC1-11 Human Male BAC"
11. 1732
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37592 a 36284 c 35592 g 35732 t
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
/10.0000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000 / 2000
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137496. .146312
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/note="assembly_fragment"
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/note="assembly_fragment"
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/db_xref="taxon:9606"
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11527: con
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5857: gap of
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ tobases 1 to 155982]
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo. sapiens, clone RP11-21E14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 10, 2000 this sequence version replaced g1:7249029.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
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8186 8285: gap of 100 bp
8286 9661: contig of 1376 bp in length
9662 9761: gap of 100 bp
9762 11131: contig of 1370 bp in length
1132 11231: gap of 100 bp
1132 57436: contig of 46205 bp in length
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71610 81113: contrig of 9504 bp in length
81114 81213: gap of 100 bp p in length
81214 92173: contrig of 10960 bp in length
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11232 57436: cont
                                                                                                                                                                          (bases 1 to 155982)
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                                                                                                                                               Unpublished
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57437
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TITLE JOURNAL

COMMENT

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AC018988 157599 bp DNA linear HTG 26-DEC-2001
Homo sapiens chromosome 15 clone RP11-233C13 map 15, *** SEQUENCING
IN PROGRESS ***, 7 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 157599)

Birran, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 15, clone RP11-233C13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy 1187 ctgcccaccttggcctcccaaagtgctgggattacaggcatgagccactgggcccagc 1244
Db 9997 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC 10054
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92174 92273: gap of 100 bp 92274 103879: contig of 11605 bp in length 103879 103978: gap of 100 bp 103979: gap of 100 bp 120092 120191: gap of 100 bp 120192 154009: contig of 13818 bp in length 154010 155982: contig of 1873 bp in length 154110 155982: contig of 1873 bp in length.
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49795 a 29060 c 29340 g 46582 t 1205 others
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1. .8185
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100.0%; Pred. No. 2.1e-21;
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65715. .71509

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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Demino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitthigh, W., Porriest, C., Gage, D., Galagan, J., Farthigh, W., Porriest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., McGurk, A., McKernan, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, C., Oconnor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Santos, R., Severy, P., Spencer, B., Stanger, Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tasfaye, S., Theodore, J., Tirrell, A., Sands, M., Viel, W., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission

Submitted (25-DE-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 26, 2001 this sequence version replaced gi:14010824.
All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L5451
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30290 30389: gap of 100 bp
30390 41503: contig of 11114 bp in length
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139274 149978: conilg of 10705 bp in length
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41604 107568: contig of 65965 bp in length
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149979 150078: gap of 100 bp
150079 157599: contrig of 7521 bp in length.
Location Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seg.wi.mit.edu
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ORIGIN
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JOURNAL
           REFERENCE
AUTHORS
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Query Match 1.8%; Score 58; DB 2; Length 157599; Best Local Similarity 100.0%; Pred. No. 2.2e-21; Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 145556 CTGCCCACCTTGGCCTCCCAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC 145613

Search completed: September 20, 2002, 06:25:43 Job time: 18137 sec

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September 20, 2002, 03:15:16 ; Search time 521.76 Seconds
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10631.997 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
                                                                                                                                                                       OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	% Query Match	% Query Match Length DB ID	DB	SUMMAKIES	Description
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7	541	16.7	1643	22	AAF24681	Nucleotide sequenc
m	541	16.7	1643	22	AAF24703	Nucleotide sequenc
4	336	10.4	763			Human cDNA clone (
S	336	10.4	1750			Human cDNA sequenc
9	228	7.1	7260			Human ATP binding
7	228	7.1	7260	22	AAI70315	Human ATP binding
8	217	6.7	736			Human cDNA clone (
σ	217	6.7	1556			Human cDNA sequenc

secreted ho ABCA1 ho Polynucl holynucl ABC1 DNA ABC1 DNA ABC1 DNA COLIGE SEGUITE SEGUI	Human nervous syst Human immune/haema Human immune/haema Human secreted pro Human secreted pro Human polynucleoti Human polynucleoti Human immune/haema Human immune/haema Human reproductive Human DNA for a no Human DNA for a no Human histone deacc	.c; cardiovascular; ABC1; ds.	N, Clee SM; lipoprotein-cholesterol
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110 1110 1110 1110 1110 1110 1110 1110	0 1 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	3 8	WO2 08- 01- 01- 15- 23- 23- (UY (XE HAY WPI
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gcaggtggtgggagttctggaatatgatggagctggaggtgggaagagaagtaggcttgg 27450

27391

(HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity -

Claim 8; Fig 1; 317pp; English.

Ø The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABCI expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.

Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;

ó; 26790 tecessasgigetigggattacaggeatgageeacigegeecageteagateeateetite 27150 tctatgggtctgtcctgagtgttgatagaaccactgatgtgagtacctgggcttgagccg 27330 tatttttttttgacacggagtcttgctctgtcactcaggctggagtgcagtggcatgatct 1021 1022 cgactcactgtaacctctgcctcccgggttcaagcgattctcctgcctcagcctcctgag 1081 1082 ataacaggcgcccaccacatctggctaatttttgtatttttagtaaagactgggttt 1141 actccagaattccttgcctggtggcctccacatgcacttccagggcctgcttgggcctct 1381 taagggcaaacagtccatggtgcaaaggggccatgccacccagagttatgagtacctggg 1321 tggcctggagatcctgttgactgtagcatggaggggcttgtgcagctgaatgtctgcat 1501 841 1502 gcaggtggtgggagttctggaatatgatggagctggaggtgggaagaggaagtaggcttgg 1561 0; Gaps 782 atgaaacagaggcagaaagactttacgtaaattgctcatcatgtggttgtcaagtttgac tctatgcgtctgtcctgagtgttgatagaaccactgatgtgagtacctgggcttgagccg 27211 actocagaattocttgcctggtggcctccacatgcacttccagggcctgcttgggcctct 25.2%; Score 814; DB 22; Length 183999; 99.7%; Pred. No. 0; 3; Indels 0; Mismatches Best Local Similarity 99.73 Matches 964; Conservative Query Match 962 27151 1322 1382 1202 27091 1262 1442 27271 g ΩD ð ò ŏ g ò g ò a ð g 셤 셤 g ò ð õ ð a ð 쉽 ð â

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27451 ggcagctctctcatgccacctcattctggccaaaactcaggtcaaactgtgaagagtcta 27510
                            aatytyaatctycccttcaayytygctacaaayytatctttytcaayytaygayacctty 1681
                                                                                                                                       Nucleotide sequence of the 5' flanking region of the human ABCl gene.
ggcagctctctcatgccacctcattctggccaaaactcaggtcaaactgtgaagagtcta
                                                                                                       AAF24681 standard; DNA; 1643 BP.
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27631 ttctatg 27637
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Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss. 99US-0140264. 99US-0153872. 99US-0166573. Garvin M; 16-JUN-2000; 2000WO-US16765. (CVTH-) CV THERAPEUTICS INC Wade D, WO200078972-A2. Homo sapiens 18-JUN-1999; 14-SEP-1999; 19-NOV-1999; 28-DEC-2000 Lawn RM,

WPI; 2001-137812/14.

Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis

Claim 1; Page 143-144; 215pp; English.

The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9422-941. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of and atherosclerosis. The genes associated with hypercholesterolemia and atherosclerosis that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for with cholesterol transport.

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        gaaggggacgcagaccgcggaccctaagacacctgctgtaccctccaccccaccccacc
        2669

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                                                                                                                                                   2190 gtaagatgttcctctcgggtcctctgagggacctggggagctcaggctgggaatctccaa 2249
                                                                                                                                                                                                                                                       are also useful as diagnostic indicators of cardiovascular disease and
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                                                                Length 1643;
                                                                                    Indels
                               Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other
      other disorders associated with hypercholesterolemia
                                                              16.7%; Score 541; DB 22; I
100.0%; Pred. No. 1.2e-236;
iive 0; Mismatches 0;
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                                                                                  Matches 541; Conservative
                                                               Query Match
Best Local Similarity
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16-JUN-2000; 2000WO-US16591.

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                                                                                                                                                                                                                                                                                                                                                            Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 138-139; 211pp; English.
                                                                                                                                                                                                                                         Garvin M;
                                                                                                                                                                                                                                         Oram JF,
                                                      99US-0153872.
                                                                                                                                            (CVTH-) CV THERAPEUTICS INC (UNIW ) UNIV WASHINGTON.
                         99US-0140264
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19-NOV-1999;
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Sequence 763 BP; 137 A; 205 C; 260 G; 158 T; 3 other;

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The present invention describes primer sets for synthesising 5602

(111-length cDNAs defined in the specification. Where a primer set

(211-length cDNAs defined in the specification. Where a primer set

(211-length cDNAs defined in the specification comprises one of

(212-comprises: (3) an oligoned sequence defined in the specification, where the

(213-complementary strand of a polynucleotide which comprises a 5'-end

(213-complementary strand of a polynucleotide which comprises a 5'-end

(213-complementary strand of a polynucleotide which comprises a 5'-end

(213-complementary strand of a polynucleotide which comprises a 5'-end

(213-complementary strand of a polynucleotide which comprises a 5'-end

(213-complementary strand of a polynucleotide which comprises a 1'-end sequence where the

(213-complementary strand of a polynucleotide complementary to a

(213-complementary strand of a polynucleotide sometheate of the 5'-end

(213-complementary strand sequence is selected from those defined in

(214-complementary). The primers are used in antisense therapy and

(3)-complementary full-length cDNAs. The primers are used in antisense therapy and

(3)-complementary full-length cDNAs. The primers are used in antisense therapy and

(4)-complementary full-length cDNAs. The primers are used in antisense therapy and

(5)-complementary full-length cDNAs. The primers allow obtaining of the full-length

(5)-complementary full-length cDNAs. The primers allow obtaining of the AHH3632

(6)-complementary full-length cDNAs. The primers allow obtaining of the full-length

(6)-complementary full-length cDNAs. The primers allow obtaining of the proteins encoded by

(7)-complementary full-length cDNAs. The primers allow obtaining of the proteins encoded by

(8)-complementary full-length cDNAs. The primers are used in the exemplification

(8)-complementary full-length cDNAs and AHH3632
                                                                                                                                                                                                                                                                                                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto J;
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Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID 1564; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                        Human cDNA clone (5'-primer) SEQ ID NO:1564.
                                                                                                                                                                                                                                        AAH04729 standard; cDNA; 763 BP.
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2000JP-0118776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000EP-0116126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1999;
27-AUG-1999;
11-JAN-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                     c 2670
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                                                                                                                              1334 c 1334
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                                                                                                                                                                                                                                                                                     AAH04729;
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AAH04729
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                                                          2896 aattgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctccc 2955
                                                                                                            gggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggcgc 3015
                                                                                                                                                            3016 tttgctccttgttttttccccggttctgttttcccccttctccggaaggcttgtcaagg 3075
                                                                                                                                                                                                              ggtaggagaaagagacgcaaacacaaaagtggaaaacaggtaaggctctccagtgact 3135
                                                                                                                                                                                                                                                             tacttgggcgttattgttttgtttcgaggccaaggaggcttcgggaagtgctcggtttcg 3195
                                                                                                                         241 tacttgggcgttattgttttgtttcgaggccaaggaggcttcgggaagtgctcggtttcg 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                  Gaps
                                                                       The present invention describes primer sets for synthesising 5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto
                                 ;
       Length 763;
                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saito K,
Otsuki 1
         Score 336; DB 22; I
Pred. No. 4.1e-143;
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                                                                                                                                                                                                                                                                                                                gggactttgatccggagccccacatccccaccactt 3231
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                                                                                                                                                                                                                                                                                                                            301 gggactttgatccggagccccacatccccactt 336
Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA sequence SEQ ID NO:16905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ota T, Isogai T, Nishikawa T, Hay
Ishii S, Sugiyama T, Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                    AAH17451 standard; cDNA; 1750 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2000; 2000EP-0116126.
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                                 Matches 336; Conservative
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                     Best Local Similarity
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27-AUG-1999;
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         Query Match
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comprises: (a) an oligo-dT primer and an oligonucleotide complementary comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprising a sequence complementary to the comprising a sequence complementary to the comprising a sequence complementary to the sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the polynucleotide which comprises a 3'-end sequence, where the polynucleotide which comprises a 3'-end sequence, where the compined which comprises a 3'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the primers are also useful for the detection and/or diagnosis of the primers allow obtaining of the full-length.
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                                                                                                                                                                                                                                                                                                                                                       cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH1842 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ATP binding cassette transporter 1; ABC1; coronary heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dermatological; atherosclerosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3016 tttgeteettgtttttteeeeggttetgtttteteeeetteteeagaaggettgteaagg 3075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3136 tacttgggcgttattgttttgtttcgaggccaaggaggtttcgggaagtgctcggtttcg 3195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2896 aattgcgagcgagagtgagtggggccgggacccgcagagccgagccgacccttctctcccc 2955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2956 gggctgcggcagggcagggcgggggagctccgcgcaccaacagagccggttctcagggcgc 3015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 tacttggggcgttattgttttgtttcgaggccaaggaggcttcgggaagtgctcggtttcg 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.4%; Score 336; DB 22; Length 1750; 100.0%; Pred. No. 4.1e-143; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1750 BP; 291 A; 489 C; 586 G; 384 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ATP binding cassette transporter 1 (ABC1) gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 336; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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The invention relates to four common polymorphisms in the gene encoding ATP-binding cassette transporter-1 (ABC1). ABC1 is associated with decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in ABC1 directly affects cellular lipid homeostasis, which is a key factor in the atherogenetic processes. The ABC1 polymorphisms are useful for diagnosing and treating lipid disorders, cardiovascular diseases (coronary heart disease, atherosclerosis) and inflammatory diseases (psoriasis, lupus erythematosus). The identification of ABC1 as a transporter for interleukin-1beta (IL-1beta) identifies this gene as a candidate for treatment of inflammatory diseases including rheumatoid arthritis and septic shock. The present sequence is human ABC1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2887 aaaccccgtaattgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccc 2946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3007 tcagggcgctttgctccttgtttttccccggttctgttttctccccttctccggaaggc 3066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2947 tteteteceegggetgeggeagggeagggegggageteegegeaceaacagageeggtte 3006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                               New adenosine triphosphate binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 aaaccccgtaattgcgagcgagagtgagtggggccgggagccgagagccgagccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ATP binding cassette transporter 1 (ABC1) cDNA.
/*tag= a
/product= "Human ABC1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 1; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI70315 standard; cDNA; 7260
                                                                                                                                 20-MAR-2000; 2000EP-0105820
                                                                                                                                                                       20-MAR-2000; 2000EP-0105820
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                                                                                                                                                                                                                                                    Schmitz G, Bodzioch M;
                                                                                                                                                                                                                                                                                         WPI; 2001-640388/74.
                                                                                                                                                                                                              (FARB ) BAYER AG.
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                                                      EP1136552-A1
                                                                                             26-SEP-2001.
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ID AAI7
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triphosphate (ATP) binding cassette transporter 1 (ABC1) protein (see AAM50227). The sequence includes an extended open reading an alternative ATC codon as initiation codon and thereby adding an alternative ATC codon as initiation codon and thereby adding an alternative ATC codon as initiation codon and thereby adding an alternative ATC codon as initiation codon and thereby adding an extra 40 N-terminal amino acids to the encoded ABC1 protein (see AAM5028). The invention provides 4 common polymorphisms in the ABC1 gene. These were identified by sequencing the ABC1 gene in different Tangler kindreds. In the variant genes (numbering as in ABC1) gene. These were identified by sequencing the ABC1 gene in different Tangler kindreds. In the variant genes (numbering as in ABC1) gene. The sequence of ABC1 and therefore position 136, As is changed to G at position 5589 or G is changed to C at position 136, and the amino acid sequence of ABC1 and therefore may affect its function. The 2 most common polymorphisms (G596A) and A2589G) are both associated with a decreased in vitro ApoA-1 mediated efflux of cholesterol from monounclear phagocytes, a stablished coronary heart disease. 3 of the variants (G596A, A2589G and G345C) are significantly increased in a population of established coronary heart disease (CHD) relative to CHD-free control subjects. The use of the provided ABC1 polymorphisms for the diagnosis and treatment of lipid disorders, cardiovascular erythematodes) is claimed, Modulation of ABC1 transcripts or protein by antisense or ribozyme technology or RNA decoys is also proved the abcops and all of the provided ABC1 transcripts or protein by antisense or ribozyme technology or RNA decoys is also
                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/note= "alternative open reading frame of AAI70314"
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Tangier disease; coronary heart disease; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
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                                                                                                                                                                                                                        Location/Qualifiers
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replace(3836,C)
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                                                                                                                                                                                                                                                                       7106
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                                               polymorphism; ss.
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                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                             Key
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Ouery Match 7.1%; Score 228; DB 22; Length 7260; Best Local Similarity 100.0%; Pred. No. 7.7e-94;

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a sequence complementary to a polynucleotide which comprises a 1'-end sequence. Where the comprises at least 15 nucleotides and the combination of the 5'-end sequence, 3'-end sequence, 3'-end sequence, 3'-end sequence, 5'-end sequence, 5'-end sequence, 5'-end sequence, 5'-end sequence, 6'-end sequence, 7'-end sequence, 6'-end seque
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                                                aaaccccgtaattgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccc 2946
                                                                                                                                                   2947 ttetetecegggetgeggeagggeagggeggggageteegegeaeeaaeagageeggtte 3006
                                                                                                                                                                                                                                                         tcagggcgctttgctccttgtttttccccggttctgttttccccttctccggaaggc 3066
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                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA clone (5'-primer) SEQ ID NO:4267.
0; Mismatches
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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Matches 228; Conservative
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02-MAY-2000;
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27-AUG-1999;
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Ishii S,
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       detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAM10316 to AAM13628 and AAM13633 to AAM18742 represent human cDNA sequences; AAB92446 to AAM595893 represent human anino acid sequences; and AAM13629 to AAM13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                        2898 ttgcgagcgagagtgagtgggccggaccgcagagccgaccttcttctcccgg 2957
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particularly full-length cDNAs. The primers are also useful for the
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Otsuki
                                                                                                                                  Sequence 736 BP; 163 A; 199 C; 199 G; 170 T; 5 other;
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                                                                                                                                                                             6.7%; Score 217; DB 22;
100.0%; Pred. No. 8.1e-89;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                             taggagaaagacgcaaacacaaaagtggaaaacag 3114
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA sequence SEQ ID NO:18808.
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                        the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-318749/34.
                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                   Query Match
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligounclectide complementary comprises one of the 5602 nucleotide sequences defined in the specification, where the complementary strand of a polynucleotide which comprises one of of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1 east 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or alignosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the complementary and complementary and an end or alignosis of the abnormality of the full-length cDNAs. The primers are also useful for the complementary and an end or alignosis of the abnormality of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs asally without any specialised methods. AAH03165 to AAH13628 and AAH086003 rowed the abnormality of AAH031628 and AAH086003 rowed the abnormality of AAH03628 and AAH0362003 rowed the abnormality of AAH03628 and AAH0362003 rowed the abnormality of AAH0362003 rowed the abnormality of AAH0362003 rowed the abnormality 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
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Matches 217; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the present invention.
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The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORP has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAS derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the MRNA because they are often obtained from oligo-dT primed cDNA ilbrarles. Such ESTS are not well suited for isolating cDNA sequences cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                        New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                  Claim 1; SEQ ID 13690; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression and secretion vectors.
                         WPI; 2000-500381/45.
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Sequence 227 BP; 44 A; 65 C; 73 G; 45 T; 0 other;

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2881 cggcaaaaaccccgtaattgcgagcgagtgagtggggccgggacccgcagagccgagc 2940
                                                                                                                                             0; Gaps
                                                                                                                        cgaccettetetecegggetgeggeagggeagggeggggggggetecegegeaceaacagage 137
                                                            h 6.5%; Score 210; DB 21; Length 227; Similarity 100.0%; Pred. No. 1.3e-85; 10; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                           3061 gaaggettgtcaaggggtaggagaaagaga 3090
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Matches 210, Conservative
Query Match
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; afherosclerosis; coronary heart disease; arterial ischaemis; bone disorder; osteoporosis; vascular growth disorder; lissue regeneration; wound healing; infection; immune disorder; artisue regeneration; wound healing; infection; immune disorder; antiarthritis; antiarthritis; antiarthritis; antiarteriosclerotic; cytostatic; osteopathic; vasctropic; cardiant; virucide; antibacterial;
                                                                                                                                                                            Human ABCAl homologue-encoding cDNA, SEQ ID NO:976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antifungal; vulnerary; antiulcer; ss.
                                            ABA09200 standard; cDNA; 7086 BP.
                                                                                                                                11-JAN-2002 (first entry)
                                                                                        ABA09200;
RESULT 11
                         ABA09200
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Homo sapiens.

current and a managed and a sequences ABA0925-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides of producing the novel polypeptides. The invention has a sample, and methods of identifying compounds which that the polypeptides of the invention although tower, many of the bind to polypeptides of the invention and though novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell differentiation activities, including cytokine, cell proliferation or cell contential therapeutic activities; stem cell growth factor activities; chemotactic or chemokinetic activities; receptor or ligand activities; or may be conditions or metastasis.

Compound the in oncogenesis, cancer cell proliferation or metastasis.

Compound the information of the preventing, treating or ameliorating medical involved in oncogenesis, center cell proliferation or ameliorating medical cancers, haematopoicate disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions, e.g., by protein or gene therapy, such conditions, e.g., by protein or gene therapy, such conditions include cancers, haematopoicated disorders (e.g., myeloid or lymphoid cell varieties in sorval, sorval, sorval, and abnormal varieties, including them) may be used to promote wound the preparation and disorders (e.g., of burns, incisions and ulcers), while those with immonodulatory activities may be used in cell survey and propeptides may be used in cell survey. Compary the companion of surfaction and product cell growth, for example, such polypeptides may be used to augment or augment of a such co autoinmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject novel human polypeptide of the invention. Claim 1; Page 833-835; 1963pp; English. Tang YT, Liu C, Drmanac RT, 05-FEB-2001; 2001WO-US03800. 03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875. e.g. arthritis and cancer -WPI; 2001-457740/49. (HYSE-) HYSEQ INC. P-PSDB; ABB11956 WO200157188-A2. 03-FEB-2000; 09-AUG-2001. 

Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

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0; Gaps
Query Match 6.3%; Score 205; DB 22; Length 7086; Best Local Similarity 100.0%; Pred. No. 2.4e-83; Matches 205; Conservative 0; Mismatches 0; Indels 0;
   Query Match
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- 2910 gigagiggggccgggacccgcagagccgagccgaccttctcccggggctgcggcaggg 2969 δ g
  - 7 gigagiggggccgggacccgcagagccgagccgaccttctctccccgggctgcggcaggg 66 δŏ
- 2970 cagggcgggagctccgcgcgcaccaacagagccggttctcaggggcgctttgctccttgttt 3029

ò g à

Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

g

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encoded polypeptides (AAM/8323-AAM/80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem ecll growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cencer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                                                          3030 tttccccggttctgttttctccccttctccggaaggcttgtcaaggggtaggagaaagag 3089
                                                                                                        cagggcggggagctccgcgccaacagagccggttctcagggcgctttgctccttgttt 126
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Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang
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Zhang J, Ren F, Chen R, Wē
?, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human polynucleotide SEQ ID NO 2196.
                                                                                                                                                                             AAK52667 standard; cDNA; 7086 BP.
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Wang J, Zhe
Wejhrman T,
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20000S-0654936.
20000S-0663561.
20000S-0693325.
20000S-0728422.
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2000US-0560875.
2000US-0598075.
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Wang D,
Yang Y, W
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20-OCT-2000;
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01-SEP-2000;
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Zhao QA,
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were missing at the time of publication

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                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoies1s; tissue growth factor; immunomodulatory; cancer; levæmid; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ma Y;
                                                                                                      2970 cagggcggggagctccgcgcaccaacagagccggttctcagggcgctttgctccttgttt 3029
                                                                                                                                                           tttccccggttctgttttctccccttctccggaaggcttgtcaagggggtaggaaagag 3089
                                                   2969
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                                                                           99
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding polypeptides with cytokine-like activities,
                                                   Xu C, Cao Y,
R, Wang ZW;
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0
Length 7086;
                          Indels
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Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
6.3%; Score 205; DB 22;
100.0%; Pred. No. 2.4e-83;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1086-1096; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                           Human polynucleotide SEQ ID NO 228.
                                                                                                                                                                                                                 3090 acgcaaacacaaaagtggaaaacag 3114
                                                                                                                                                                                                                                AAK51683 standard; cDNA; 7281
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2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0663361.
2000US-0663361.
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Query Match 6.3
Best Local Similarity 100.
Matches 205; Conservative
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15-SEP-2000; 2
20-OCT-2000; 2
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production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, wematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s M, Arnould-Reguigne I, Prades C, Naudin L;
Jaye M, Searfoss GH, Remaley A, Brewer HB;
                                                                                                                        Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                           2970 cagggcggggagctccgcgcaccaacagagccggttctcagggcgctttgctccttgttt 3029
                                                                                                                                                                                                                                                                                                                            45 gtgagtggggccgggacccgcagagccgagccgaccttctctcccgggctgcggcaggg 104
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
                                                                                                                                                                                                                                                                                                 9t9a9t9g9gccgggacccgcagagccgagccgaccttctccccgggctgcggcaggg
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                                                                                                                                                                                                                                    6.3%; Score 205; DB 22;
100.0%; Pred. No. 2.4e-83;
7ative 0; Mismatches 0;
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Duverger N, Jaye
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01-MAR-2000; 2000US-0186260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ABC1 DNA sequence #2.
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                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 205;
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                                                                                                             inflammation
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Lemoine C,
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nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3030 tttccccggttctgttttctccccttctccggaaggcttgtcaaggggtaggagaagag
                                                                                                                     The sequence represents the coding sequence #2 of human ABC1. The
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                                                                                                                                                                                                                                                                         pathologies, and other diseases e.g. Tangier disease, lecithin-
cholesterol (LCAT) deficiency, malaria and diabetes.
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                                 New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes – \,
                                                                                                                                                                                                                                                                                                                             Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;
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100.0%; Pred. No. 2.4e-83;
iive 0; Mismatches 0;
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                                                                                 Claim 1; Page 209-213; 368pp; English.
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P-PSDB; AAU02176.
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14-SEP-1999;
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                                                                                                                                                              Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
                                                                                                                                                                                                                                                                                                       present sequence encodes a human adenosine triphosphate (ATP)
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100.0%; Pred. No. 1.1e-79;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                               Disclosure; Page 122-128; 215pp; English.
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99US-0166573,
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197; Conservative
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binding casette protein (ABC) I polypeptide. ABCI resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABCI is defective in Tanglar disease, a genetic disorder stores. ABCI is defective in Tanglar disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 942.9431. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and the disorders associated with hypercholesterolemia.
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100.0%; Pred. No. 1.1e-79;
tive 0; Mismatches 0;
                  /*tag= a
/product= "ABC1 polypeptide"
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                                                                                                                                                                                               99US-0153872.
99US-0166573.
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                                                                                                                                            16-JUN-2000; 2000WO-US16591
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19-NOV-1999;
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The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide, and is isolated from a Tangler disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangler disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders
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                                                                       Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                                                                                                                               apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
chromosome 9q22-9q31; heart disease; hypercholesterolemia;
atherosclerosis; cholesterol transport; ss.
                                                                                                            Human; adenosine triphosphate binding cassette protein 1; ABC1;
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                                                                                                                                                                                                                                                                                              /product= "defective ABC1 polypeptide"
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323..7108
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99US-0153872.
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 AAF24685;
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 5.8%; Score 188; DB 22; Length 10474;
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          Pred. No. 1.4e-75;
     100.0%; Prec. ...
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Query Match
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Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

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binding cassergation (ABC) I polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other
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Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                                                                                                                                                                                                                                                                                                                                Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
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19-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) I polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the
                                                                                                                      2987 cgcaccaacagagccggttctcagggcgctttgctccttgtttttccccggttctgttt 3046
                                                                                                                                                                                  tctccccttctccggaaggcttgtcaagggtaggagaaagagacgcaaacacaaaagtg 3106
                                                            2927 ccgcagagccgagccgaccttctcccgggctgcggcagggcagggcgggggagctccg 2986
                                                                            102 cycaccaacagayccgyttctcaygycyctttyctccttytttttccccgyttctyttt 161
                                                                                                                                                                                                                 162 totococttotocogaaaggottgtcaaaggggtaagaaaaaaagagacaaaacacaaaagtg 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                               Gaps
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5.8%; Score 188; DB 22;
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iive 0; Mismatches 0;
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99US-0166573.
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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/*tag= a
                              Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-137811/14.
P-PSDB; AAB31366.
                 Similarity
                                                                                                                                                                                                                                                 gaaaacag 3114
                                                                                                                                                                                                                                                                            222 gaaaacag 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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   Query Match
                   Local
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plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
            mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal FDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9422-9431. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders
                                                                                                                                                                                                                                                                                                                              egeaceaacagageeggtteteagggegetttgetecttgttttteeeeggttetgttt 3046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tctccccttctccggaaggcttgtcaaggggtaggagaaagagagcgcaaacacaaaagtg 3106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 cgcaccaacagagccggttctcagggcgctttgctccttgtttttccccggttctgttt 161
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; adenosine triphosphate binding cassette protein 1; ABCl; apoliopprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                               Length 10474;
                                                                                                                                                                                                               Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "defective ABC1 polypeptide"
                                                                                                                                                                                                                                                               Ouery Match 5.8%; Score 188; DB 22; Best Local Similarity 100.0%; Pred. No. 1.4e-75; Matches 188; Conservative 0; Mismatches 0;
                                                                                                                                                                                associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 323..7108
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99US-0153872.
99US-0166573.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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14-SEP-1999;
19-NOV-1999;
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Garvin M;

Oram JF,

Wade D,

Lawn RM,

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The present sequence encodes a human adenosine triphosphate (ATP)
binding cassette protein (ABC) 1 polypeptide, and is isolated from
a Tangler disease patient. ABC1 resides in cell membranes and utilises
ATP hydrolysis to transport a wide variety of substrates across the
plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
compolitation of intracellular cholesterol stores. ABC1 is defective in
Tangler disease, a genetic disorder characterised by abnormal
HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
of 9422-9431. The ABC1 genes and proteins are useful for developing
pharmaceutical agents for the treatment of heart disease and other
disorders associated with hyperchlossterolemia and atherosclerosis. The
genes are useful for developing screening assays to screen for compounds
transport. The genes and proteins are also useful
c as diagnostic indicators of cardiovascular disease and other disorders
                                                                 Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3047 tctccccttctccggaaggcttgtcaaggggtaggagaaagagacgcaaacacaaaagtg 3106
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cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.8%; Score 188; DB 22; Length 10474;
100.0%; Pred. No. 1.4e-75;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;
                                                                                                                                                        Claim 30; Page 165-172; 211pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated with hypercholesterolemia.
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Matches 188; Conservative
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                2001-137811/14.
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                                                                                                                        atherosclerosis -
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polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABCI gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological pathologies, and other diseases e.g. Tangler disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                    Brewer HB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3023 cttgtttttccccggttctgttttcccccttctccggaaggcttgtcaaggggtagga 3082
                                                                                                                                                                                                                                                                                                                                                     The sequence represents the partial coding sequence of human ABC1, which encodes amino acids 1-60 of the human ABC1 protein. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, ABC1 gene; atherosclerosis; reverse transport; cholesterol;
cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
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Duverger N, Jaye M, Searfoss GH, Remaley A, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.8%; Score 92; DB 22; Length 446;
                                                                                                                                                                                                                                                                           New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 8.8e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. ....
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185..6967
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                                                          26-OCT-2000; 2000WO-EP10886.
                                                                                                        01-MAR-2000; 2000US-0186260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ABC1 DNA sequence #1.
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                                                                                                                                         (AVET ) AVENTIS PHARMA SA.
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Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
                                                                                                                                                                                                                                 WPI; 2001-316327/33.
                                                                                                                                                                                                                                              P-PSDB; AAU02176
WO200130848-A2.
                                                                                           26-OCT-1999;
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                              03-MAY-2001.
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Lemoine C,
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AAV57903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                3023 cttgtttttccccggttctgttttctccccttctccggaaggcttgtcaaggggtagga 3082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
                                                                                                                                   Brewer HB
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hereditary haemochromatosis subregion from an unaffected individual.
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                                                                                                                        Prades C,
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9741;
                                                                                                                     Rosier-Montus M, Arnould-Reguigne I, Prades (
Duverger N, Jaye M, Searfoss GH, Remaley A,
                                                                                                                                                                                                New human ABC1 nucleic acids and polypeptides for treating
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                     2.8%; Score 92; DB 22; Length 97
100.0%; Pred. No. 8.6e-32;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3083 gaaagagacgcaaacacaaaagtggaaaacag 3114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis, malaria and diabetes
                                                                                                                                                                                                                               Claim 1; Page 204-208; 368pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV57926 standard; DNA; 235033 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             type 1 sodium transport gene; ss.
                                          26-OCT-2000; 2000WO-EP10886
                                                               26-OCT-1999; 99EP-0402668.
01-MAR-2000; 2000US-0186260.
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                                                                                                (AVET ) AVENTIS PHARMA SA.
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nes 92; Conservative
                                                                                                                                                                 2001-316327/33.
                                                                                                                                                                           P-PSDB; AAU02176
WO200130848-A2
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                     03-MAY-2001
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Lemoine C,
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                                                                                                                                            Dean M;
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Matches
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products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis (HH). Also described is a unaffected by hereditary haemochromatosis (HH). Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HHE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence or absence of a haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genotype indicates the likely presence of the HFE gene mutation in which are benologues of the milk HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BFF genes, which are homologues of the milk protein butyrophilin (HF), and can be used in the production of agonists and antagonists of BF function. Also described are: (1) a RoRet gene which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NFT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
                                                                                                                                                                                                                                                                                                                                                                     Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1190 cccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes hereditary haemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 235033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                      Thomas WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.4e-15;
hes 0;
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100.0%; Pred. No. 6.4e-15
tive 0; Mismatches 0
                                                                                                                                                                                          Lauer PM, Ruddy DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarly be used for hypophosphatemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV57903 standard; DNA; 237326 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type 1 sodium transport gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 8; 209pp; English.
97US-0852495
96US-0724394
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Best Local Similarity 100.0
Matches 55; Conservative
                                                                                                                                                                                                                         rsuchihashi Z, Wolff RK;
                                                                                                                (PROG-) PROGENTIOR INC.
                                                                                                                                                                                          Kronmal GS,
                                                                                                                                                                                                                                                                                               WPI; 1998-240014/21
07-MAY-1997;
01-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   metabolism
                                                                                                                                                                                          eder JN,
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products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis subregion from an hereditary haemochromatosis subregion from an hereditary haemochromatosis (HH) affected individual. Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BFF genes, which are homologues of the milk conducts to the used in the production of agonists and antagonists of BFF function. Also described are: (1) a RoRet gene and antagonists of develop products for the study, diagnosis and treatment of lupus and slogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                 Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ribosomal S11 protein 12; cytostatic; virucidal;
immunomodulatory; antiinflammatory; haemostatic; malignant tumour;
human immunodeficiency virus; HIV; infection; immunological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 227302 cccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 227356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1190 cccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 1244
                                                                                                                                                                                                                                                                                                           The present invention describes hereditary haemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T; 0 other;
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0
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                                                                                  Thomas WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "ribosomal S11 protein 12"
/note= "claimed in claim 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
1.7%; Score 55; DB 19; I
Best Local Similarity 100.0%; Pred. No. 6.4e-15;
Matches 55; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ribosomal S11 protein 12 encoding cDNA.
                                                                                  Ruddy DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarly be used for hypophosphatemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
643..969
                                                                                Lauer PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI64613 standard; cDNA; 1316 BP
                                                                                                                                                                                                                                                               Claim 1; Fig 9; 209pp; English.
  96US-0724394.
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                                                                                Feder JN, Kronmal GS, La
Tsuchihashi Z, Wolff RK;
                                        (PROG-) PROGENTIOR INC.
                                                                                                                                           WPI; 1998-240014/21.
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01-OCT-1996;
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                                                                                                                                                                                                                               metabolism
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ID AAI6
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Human; secreted extracellular matrix protein; ds; immunomodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzhelmers; immune/autoimmune disease; HIV infection; anaemia;
                                                                                                                                                                                                                                                                                                          The invention relates to the human ribosomal S11 protein 12 with cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic activity. The protein and encoding polynucleotide are used in diagnosis and treatment of malignant tumour, haemopathy, human immunodeficiency virus (HIV) infection, immunological diseases and various inflammations. The polynucleotide is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
                                                                                                                                                                                                            applicable in diagnosis and treatment of malignant tumour, haemopathy, human immunodeficiency virus infection, immunological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human DNA for a novel extracellular matrix protein, Seq ID No 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human ribosomal S11 protein 12 and encoded polynucleotide,
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Pred. No. 1.5e-13;
0; Mismatches 0;
                                                                             (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                               Claim 6; Page 29-30; 34pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.6%; Sccilarity 100.0%; Pi
Conservative 0;
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ID AAS31466 standard; DNA; 5351 BP.
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20000S-0184664.
20000S-0186350.
20000S-0189874.
20000S-0199076.
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            26-MAR-2001; 2001WO-CN00438
                                              27-MAR-2000; 2000CN-0115182.
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                                                                                                                                              WPI; 2001-597104/67.
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nes 52; Conserv
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                                                                                                               Mao Y, Xie Y;
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02 - MAR - 2000;
16 - MAR - 2000;
17 - MAR - 2000;
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Best Local S
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18-APR-2000; 2000US-0198123.
19-MAY-2000; 2000US-0205515.
07-JUN-2000; 2000US-0215457.
28-JUN-2000; 2000US-0215457.
28-JUN-2000; 2000US-0216457.
07-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0217487.
14-AUG-2000; 2000US-0225214.
14-AUG-2000; 2000US-0225216.
14-AUG-2000; 2000US-0225267.
14-AUG-2000; 2000US-022527.
14-AUG-2000; 2000US-02257.
14-AUG-2000; 2000US-02257.
16-SEP-2000; 2000US-0229345.
01-SEP-2000; 2000US-0229345.
05-SEP-2000; 2000US-0229347.
06-SEP-2000; 2000US-0229397.
06-SEP-2000; 2000US-0231243.
08-SEP-2000; 2000US-0232397.
14-SEP-2000; 2000US-0232397.
14-SEP-2000; 2000US-0232397.
14-SEP-2000; 2000US-0232397.
14-SEP-2000; 2000US-0232397.
14-SEP-2000; 2000US-0232399.
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2000US-0234274.
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2000US-0235484
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02-OCT-2000;
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13-OCT-2000;
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2000US-0246526.
2000US-0246527.
2000US-0246528.
2000US-0246503.
2000US-0246609.
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2000US-0241809.
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2000US-0249244
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2000US-0251990
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2000US-0246524
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(HUMA-) HUMAN GENOME SCI INC

Ruben SM Rosen CA, Barash SC,

WPI; 2001-465572/50

Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -

Claim 1; SEQ ID No 545; 577pp; English.

The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical

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condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides comey also be used as DNA probes in diagnostic assays. The SPs may also be used as natigens to produce antibodies and to identify modulators of antagonists and antagonists) of the SPs. The anti-(SP) antibodies and can antagonists of the CPs. The anti-(SP) antibodies and contagonists may also be used to down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. cardiac melanomas, neoplasms of the breast or liver, Sezary syndrome and parkninson's disease), neurological diseases (e.g. Alzheimer's disease).

Caucher's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses include wound healing, maintenance of organs before transplantation, support of cell culture of primary tissues, modulation of for example
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Similarity 100.0%; Pred. No. 1.5e-13;
52; Conservative 0; Mismatches 0; Indels (
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The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPs may also be
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          agonists and antagonists) of the SPs. The anti-(SP) antibodies and antagonists may also be used to down regulate expression and activity of sp and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation, support of cell culture of primary tissues, modulation of for example
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used as antigens to produce antibodies and to identify modulators
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Best Local Similarity 100.0%; Pred. No. 1.5e-13;
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anino acid sequences given in Amagalin influential inf
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Gaps

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24-FEB-2000;
02-MAR-2000;
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26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; imunosouppressive; antiliflammatory; antil-HTV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarhritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antilnflammatory; antialhergic; antidiabetic; antilucer; anticonvulsant; antimingal; antiparastitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                 number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
                                                                                                                                                                                                                                       reproductive system antigen
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of a
                                                                                                                                                                                                                                               used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 5924; 1297pp + Sequence Listing; English.
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1.5e-13;
hes 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                     Sequence 10901 BP; 3320 A; 2001 C; 2044 G; 3536 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 1.6%; Score 52; DB
100.0%; Pred. No. 1.5
/ative 0; Mismatches
                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a
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                                                                                                                                                                                              Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                            2000US-0250160.
2000US-0250391.
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          2000US-0249299.
2000US-0249300.
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2000US-0251988.
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2000US-0251990.
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2000US-0251856
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2000US-0251869
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                                                                                                                                                                                                                                                                                                                                  protein of the invention.
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Best Local Similarity 100.
Matches 52; Conservative
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2000US-0184664.
2000US-0186350.
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2000US-019076.
2000US-020515.
2000US-0209467.
2000US-0209467.
2000US-021886.
2000US-021647.
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2000US-0220963.
2000US-0220964.
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2000US-0224519.
2000US-0225213.
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2000US-0217496.
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2000US-0225447.
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20000S-0225759.
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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
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2000US-0249212.
2000US-0249213.
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000US-0251868.
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2000US-0249207
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                                                 13-OCT-2000;
20-OCT-2000;
20-OC
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestianl tract, liver, lung, or urogenital; (b) immune discrders e.g. Addison's disease, alleriques, autoimmune champing autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections diseases such as viral, bacterial, fungal
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                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Disclosure; SEQ ID NO 10357; 1701pp + Sequence Listing; English.
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Pred. No. 1.5e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;
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2000US-0209467.
2000US-0214886.
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2000US-0216647.
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2000US-0189874.
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2000US-0184664
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28-JUN-2000;
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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -

Disclosure; SEQ ID NO 12842; 1701pp + Sequence Listing; English

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune discorders e.g. addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative

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colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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AMK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cativity, and can be used in gane therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased cypression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nuclear acids into a host cell and culturing the cell to express the corotine. (I) proteins and polynucleotides may be used to prevent, additionally concers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic-derived cells. AAK64703 concers are researt invention. AAK54912 to AAK87950 and AAM82169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 25603; 3071pp + Sequence Listing; English.
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2000US-0246476.
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2000US-0246477.
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20000S-0246524
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200005-0249210.
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200005-0249213.
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20000S-0249218.
20000S-024924.
20000S-0249245.
20000S-0249265.
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20000S-0236369.
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20000S-0236802.
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2000US-0250160
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-NOV-2000;
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25-SEP-2000;
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27-SEP-2000;
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13-OCT-2000;
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08-NOV-2000;
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08-NOV-2000;
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08-NOV-2000;
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17-NOV-2000;
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02-OCT-2000;
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20-OCT-2000;
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20-OCT-2000;
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01-NOV-2000;
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L7-NOV-2000;
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02-OCT-2000;
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cartivity, and can be used in AMM81710 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expression in a patient's genome that affect the activity of (I) by expression of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting protein. (I) proteins and polynucleotides may be used to produce the real timenne/haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic-derived cells. AAK64703 concers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK49421 to AAK87690 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 33324; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein 5' EST, SEQ ID NO: 30024.
                                                                                                                                                                                                                                                                     Rosen CA, Barash SC, Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC25949/c
ID AAC25949 standard; cDNA; 149
             2000US-0251030.
2000US-0251988.
2000US-0251479.
200US-0251856.
200US-0251868.
2000US-0251869.
                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                          2000US-0251990.
2000US-0254097.
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                                                                                                                                                                                                                                                                                                       WPI; 2001-483426/52.
             05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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11-DEC-2000;
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06-SEP-2000

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2001-514838/56
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                          P-PSDB; AAO01722
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                                                                           disorders
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                                                                                                                                                                                                    The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                              New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
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                                                                                  Duclert A, Giordano J;
                                                                                                                                                                              Claim 1; SEQ ID 30024; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polynucleotide SEQ ID NO 1713.
                                                                                                                                                                                                                                                                                                                                                                expression and secretion vectors.
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          21-FEB-2000; 2000EP-0200610.
                                  99US-0122487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Conservative
                                                                                 Dumas Milne Edwards J,
                                                                                                         WPI; 2000-500381/45.
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                                                          (GEST ) GENSET
                                  26-FEB-1999;
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA009310) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
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ID AA187958 standard; cDNA; 425
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08-NOV-2000;
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05-SEP-2000;
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29-SEP-2000
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                        The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                    Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                  Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32733.
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2000US-0209467.
2000US-0214886.
2000US-0215135.
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2000US-0224519.
2000US-0225213.
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2000US-0218290.
2000US-0220963.
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2000US-0189874.
2000US-0190076.
2000US-0198123.
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2000US-0217487
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                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 51; Conservative
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16-MAR-2000;
17-MAR-2000;
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07-JUL-2000;
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11-JUL-2000;
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14-JUL-2000;
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24-FEB-2000;
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2000US-0229344.
2000US-0229345.
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2000US-0229513.
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2000US-0241809.
2000US-0241826.
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2000US-0241785
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2000US-0241787
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2000US-0246524
                     14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
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29-SEP-2000;
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ANX54951 to AAX64702 encode the human immune/haematopoietic antigen (1)

C amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)

proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)

C supplement the patients own production of (I). Additionally, (I)

C polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AAK64703

C cancers and cancer metastases of haematopoietic antigen genomic
c cancers and cancer metastases of haematopoietic antigen genomic
c sequences from the present invention. AAK54942 to AAK87650 and AAM82169

C represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 32733; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0250160.
2000US-0250391.
2000US-0251030.
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2000US-0249212.
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2000US-0249245.
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                            Gaps
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                                                                      Length 1856;
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/*tag= a
/product= polypeptide-cytochrome b5-13"
/note= "claimed in claim 6"
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                                                                                                                                                                                                                                      Human polypeptide-cytochrome b5-13 encoding cDNA.
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100.0%; Pred. No. 4.4e-13;
Live 0; Mismatches 0;
               4.4e-13;
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  DB 22;
 1.6%; Score 51; DB 100.0%; Pred. No. 4.4 ative 0; Mismatches
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                              Conservative
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Matches 51; Conservative
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 Query Match
Best Local Similarity
Matches 51; Conserv
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RESULT 3

Sequence 1856 BP; 375 A; 416 C; 358 G; 707 T; 0 other;

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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0232397.
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2000US-0231242
                                 (first entry)
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04-FEB-2000;
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PR 14-SEP-2000; 2000US-0232399.
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PR 21-SEP-2000; 2000US-0233405.
PR 21-SEP-2000; 2000US-0233405.
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PR 22-SEP-2000; 2000US-0233436.
PR 22-SEP-2000; 2000US-0233436.
PR 23-SEP-2000; 2000US-0234478.
PR 20-OCT-2000; 2000US-0244475.
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PR 20-OCT-2000; 2000US-02
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17-JAN-2001; 2001WO-US01345
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                                                            24-FEB-2000;
and AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to provent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK87695 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuocer; vulnerary; anticonvulsant; antidecterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ds.
                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                                                                                   Rosen CA, Barash SC, Ruben SM;
           06-DEC-2000; 2000US-0251479.

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  2000US-0256719
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WPI; 2001-488786/53

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The invention relates to novel genes (ABA07454-ABA08224) and proteins (ABB10743-ABB10980) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune chaemaly, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple solerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
New isolated ovarian and/or breast cancer related nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders, particularly ovarian and/or breast cancer -
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                                                               Disclosure; SEQ ID NO 708; 577pp + Sequence Listing; English.
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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Gaps

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Indels

Query Match 1.6%; Score 51; DB 22; I Best Local Similarity 100.0%; Pred. No. 4.4e-13; Matches 51; Conservative 0; Mismatches 0;

Length 17904;

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08-SEP-2000; 2
08-SEP-2000; 2
14-SEP-2000; 2
15-SEP-2000; 2
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27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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02-0CT-2000;
13-0CT-2000;
20-0CT-2000;
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20-0CT-2000;
20-0CT-2000;
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20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
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02-OCT-2000;
02-OCT-2000;
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29-SEP-2000;
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17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 paraitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.4e-13;
hes 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                    2000US-0249265.
2000US-0249297.
                                                                                                      2000US-0249300.
2000US-0250160.
                                                                                   2000US-0249299
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2000US-0251479
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                                     2000US-0249264
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                                                                               17 NOV 2000;
17 NOV 2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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Human; foetal tissue antigen; ds; antiinflammatory; neuroprotective; immunomodulator; cardiovascular; cytostatic; nephrothropic;
                                               cardiovascular; autoimmune disease; rhematoid arthritis; hyperproliferative disorder; breast neoplasm; cancer; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cardiocarrest; cerebrovascular disorder; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; food additive.
         Human DNA for a novel foetal antigen, SEQ ID No 1846.
                                                                                                                                                                                                                                                                     2000US-0198123.
2000US-0205515.
2000US-0209467.
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2000US-0215135.
2000US-0216647.
2000US-0216880.
2000US-0217487.
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2000US-0225270.
2000US-0225447.
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2000US-0225758.
2000US-0225759.
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2000US-0226681.
2000US-0226868.
2000US-0227009.
2000US-0228924.
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2000US-0225266.
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2000US-0224519.
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                                                                                                                                           WO200155312-A2.
                                                                                                                          Homo sapiens.
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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19-MAY-2000;
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24-FEB-2000;
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14-AUG-2000;
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14-AUG-2000;
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2000US-0232397

AAS34422 standard; DNA; 32186 BP

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RESULT 43 AAS34422 17-DEC-2001 (first entry)

AAS34422;

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25-SEP-2000; 2000US-0235484.
27-SEP-2000; 2000US-0235484.
27-SEP-2000; 2000US-0235484.
29-SEP-2000; 2000US-0235334.
29-SEP-2000; 2000US-0236367.
29-SEP-2000; 2000US-0236367.
29-SEP-2000; 2000US-0236367.
29-SEP-2000; 2000US-0236370.
02-OCT-2000; 2000US-0237037.
02-OCT-2000; 2000US-0237037.
02-OCT-2000; 2000US-0237038.
02-OCT-2000; 2000US-0237038.
02-OCT-2000; 2000US-0237038.
02-OCT-2000; 2000US-0237038.
03-OCT-2000; 2000US-0237040.
03-OCT-2000; 2000US-0237040.
03-OCT-2000; 2000US-0241808.
03-OCT-2000; 2000US-0246475.
03-NOV-2000; 2000US-024652.
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2000US-0246610.
2000US-0246611.
2000US-0246613.
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2000US-0249211.
2000US-0249212.
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                                                                  2000US-0233064
                                                                                   2000US-0233065
                                       14-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
21-SEP-2000; 2
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17 - NOV - 2000;
17 - NOV - 2000;
                                                                                                               21-SEP-2000;
25-SEP-2000;
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The invention relates to novel nucleic acids encoding novel human foetal antigens. The nucleic acids and proteins are used to prevent, treat (e.g. antigens. The nucleic acids and proteins are used to prevent, treat (e.g. rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to the antigens can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radoimmunoassays or enzyme linked immunoassays (BLISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritiss, include autoimmune diseases e.g. rheumatoid arthritiss, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. The polypeptides can also and ocular disorders e.g. corneal infection. The polypeptides can also be prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to repenerate tissues and in fomotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, contents, content, lipid, protein, carbohydrate, vitamins, contents, content, lipid, protein, carbohydrate, vitamins, contents, content, lipid, protein, carbohydrate, vitamins, and content, lipid, protein, earbohydrate, vitamins, and contents that a disperse transplantations and other nutritional compensations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins are given in the specification. The present sequence is a genomic DNA fragment from a gene encoding a foetal antigen of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           examples of diseases and disorders treated by the nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thioredoxin reductase; TxR; human; inflammation; cancer; apoptosis; X-linked inhibitor of apoptosis protein binding protein; XIAP; viral infection; chromosome 22q11.2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides and polypeptides for diagnosing, treating, preventing or prognosing e.g. diseases or disorders of the nervous, musculoskeletal, excretory, gastrointestinal, reproductive, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human thioredoxin reductase (TxR) genomic DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID No 1846; 642pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA53450 standard; DNA; 66566 BP
                                                                                                                                                                                                                                                                                                                                    Rosen CA, Barash SC, Ruben SM;
05-DEC-2000; 2000US-0251988.
06-DEC-2000; 2000US-0256719.
06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251999.
                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                         11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                respiratory systems
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                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic nucleotide sequence. The invention relates to two TxR proteins, which have XIAP (X-linked inhibitor of apoptosis protein)-binding protein activity. The human TxR gene is located on chromosome 22q11.2. The invention includes antibodies which bind to the proteins, a vector containing the TxR encoding nucleotide sequences, and methods for producing transformants using the vector. Thioredoxin reductase has cytostatic and anti-inflammatory activity, and is used in the treatment of diseases relating to apoptosis particularly due to cancer of viral infection. TxR can also be used to treat inflammation and in the
                                                                                                                                                                                                                                                                                                                  (XIAP)-binding protein), with thioredoxin reductase activity, useful e.g. for treating apoptosis-related disorders, cancer and inflammation
                                                                                                                                                                                                                                                                                             Thioredoxin reductase II (an X-linked inhibitor for apoptosis protein
                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a human thioredoxin reductase (TxR) encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                    (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 74-135; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      screening of anti-cancer agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC89560 standard; DNA; 122186
                                                                                                              99WO-JP05983
                                                                                                                                                 98JP-0310422
                                                                                                                                                                                                                         Toji S, Yano M, Tamai K;
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Matches 51; Conservative
                                                                                                                                                                                                                                                            WPI; 2000-365627/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HDAC-D; cell cyc
gene therapy; ds
                                    WO200026382-A1.
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 Homo sapiens.
                                                                                                            28-OCT-1999;
                                                                                                                                                 30-0CT-1998;
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03-MAY-1999;

30-NOV-2000,

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The present invention provides inhibitors of histone deacetylase enzymes such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These inhibitors may be antisense strands or they may be compounds identified by contacting the enzyme with the compound and measuring the resulting enzyme activity. These inhibitors are useful for treating cancers and for identifying which histone deacetylase is involved in a neoplasia.
                                                                                                    deacetylase, useful for treating and/or alleviating the symptoms of neoplasia, or for inhibiting neoplastic cell growth in an animal -
                                                                                                                                                                                                                                                                                                                                              Sequence 122186 BP; 29016 A; 31077 C; 32425 G; 29668 T; 0 other;
                                                                              Antisense oligonucleotide that inhibits expression of a histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 122186;
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 51; DB 22; I
Pred. No. 4.3e-13;
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100.0%; Pred. No. %...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: September 20, 2002, 06:06:55 Job time: 10299 sec
                                                                                                                                                             Disclosure; Page 89-125; 125pp; English.
Macleod AR, Li Z, Besterman JM;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.69
Best Local Similarity 100.0
Matches 51; Conservative
                                        WPI; 2001-016407/02.
  99US-0132287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-2000; 2000WO-IB01252.
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Gaps

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 03:09:41; Search time 111.56 Seconds (without alignments)

Title: US-09-846-456-1

Perfect score: 3231
Sequence: 1 acagggcatggtggcaggtg......gccccacatccccacctt 3231
Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0
Searched: 383533 seqs, 122816752 residues
```

Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

0

Word size :

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/bcTUS\_COMB.seq:\*
6: /cgn2\_6/ptodata/2/ina/bcTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		•				SUMMAKIES	
Result			>.	:			-
S.	Score	e Match	<u>.</u>	Length DB	р В :	ID	Description
υ		55 1.	7	246240	7	US-08-724-394A-20	Sequence 20, Appl
U	7	7		46240	7	US-08-724-394A-21	
ပ	<u>س</u>	55 1.	r.	246240	7	US-08-724-394A-22	22,
	7	1		31571	Н	US-08-323-443B-1	Sequence 1, Appli
	2	18 1.		53526	e	US-08-658-136-2	Sequence 2, Appli
	9			53577	٣	US-08-658-136-1	
	7	17 1.		13158	7	US-08-687-080-105	105
O	8	1	₹.	153	7	US-08-849-701-2	Sequence 2, Appli
U	6		1.4	891	4	US-09-247-155-141	147
	10		4	1701	4	US-09-078-294-9	Sequence 9, Appli
	11	7	4	3267	7	US-08-257-963B-12	Sequence 12, Appl
	12 '		1.4	3267	4	US-08-367-841A-12	12,
	13		1.4	3267	Ŋ	PCT-US95-07201-12	Sequence 12, Appl
υ	14 ,	45 1.	4	3663	4	US-09-499-884-11	11,
ט	15 '	П	4.	5581	4	US-08-973-544-1	Sequence 1, Appli
	16	П	4	8409	4	US-09-167-681-37	
	17	П	4.	22481	4	US-08-367-841A-43	
	18	П	₹.	22481	S	PCT-US95-07201-43	Sequence 43, Appl
	19	1	4.	84495	4	US-09-797-906-3	Sequence 3, Appli
	70	45 1.	4	246240	7	US-08-724-394A-20	Sequence 20, Appl
	21	45 1.	4	246240	7	3	
	22	1	4	246240	7	US-08-724-394A-22	22,
υ	23	1	4.	176373	3	US-09-128-155-17	17,
ပ	24	43 1.	ĸ.	2310	Н	US-08-471-570-9	6
υ	25	43 1.	٣.	2676	+	US-08-471-570-7	7
	. 56	43 1.	٣.	14796	4	US-08-975-080-35	
	27	43 1.	۳.	14796	4	US-09-630-706-10	Sequence 10, Appl

, Appli , Appl
sednence Sed
US-09-496-694B-3 US-09-341-587-7 US-09-341-587-7 US-08-812-204-1 US-08-812-204-1 US-08-846-981-2 PCT-US93-11915-2 US-08-324-465-5 US-08-324-465-5 US-08-324-465-5 US-08-324-465-5 US-08-324-465-5 US-08-324-465-5 US-08-324-465-1 US-09-121-29 US-09-121-29 US-09-121-207 US-09-121-4-698-107 US-09-121-4-698-107 US-09-121-496-841C-103
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14796 28720 72604 16156 1656 1656 1725 1725 1725 1725 1726 198 198 198 198
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## ALIGNMENTS

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US-08-724-394A-20/C
US-08-724-394A-20/C
US-08-724-394A-20/C
Sequence 20, Application US/08724394A

Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Freder, John N.
APPLICANT: Tauchhashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Sequences and Antibodies Thereto
TITLE OF INVENTION: Sequences and Antibodies Thereto
TITLE OF INVENTION: Sequences and Antibodies Thereto
CORRESPONDENCE ADDRESS:
ADDRESSE: TOWENTION: Sequences and Antibodies Thereto
CITY: San Francisco
COMPUTER: TEN POCOMPATION: Sequences #1.0, Version #1.30
CURREST APPLICATION DATA:
COMPUTER: Patentin Release #1.0, Version #1.30
CURREST APPLICATION NUMBER: US/08/724,394A
FILING DATE: U-CCT-1996
CLASSIFICHATION NUMBER: 35,136
RESTRANCE/OCKET NUMBER: 017957-000100
TELEPAN: ELECHANCIENTION: Sequence
SEQUENCE CHARACTERISTICS:
LENGTH: A15-576-0300
INPORMATION FOR SED ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: A15-576-0300
INPORMATION FOR SED ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: A15-576-0300
INPORMATION: 1.246240 base pairs
FRAUBE:
NAME/KEY: misc_feature
LOCATION: 1.246240
LOCATION: 1.246240
LOCATION: A124544.
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US-08-724-394A-22/C

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                                                                                                             Db 14447 CCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGGGCCCAGC 14393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1190 cccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
Query Match 1.7%; Score 55; DB 2; Length 246240; Best Local Similarity 100.0%; Pred. No. 5.1e-15; Matches 55; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 246240;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Megabase Transcript Map: No. 5872237el
Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.7%; Score 55; DB 2; Length 246.
100.0%; Pred. No. 5.1e-15;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFILGA.

ATTORNEY/AGENT INFORMAL.

NAME: FILES, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 017957-000100

TELECHMUNICATION INFORMATION:

TELEFAX: 415-576-0300

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 246240 base pairs

TYPE: not relevant

CADNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-0CT-1996 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                               Sequence 21, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Reder, John N.
                                                                                                                                                                                                                                                                                                                         Gregory S.
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase T
ITLE OF INVENTION: Sequences
                                                                                                                                                                                                                                                                                                                                      Lauer, Peter M.
Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                       Kronmal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                        RESULT 2
US-08-724-394A-21/C
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                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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Gaps
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 246240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: U0-0CT-1996
CLASSIFICATION: 536
ATTONNEY/AGENT INFORMATION:
NAME: Fitts, Renea 35,136
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
TELEPROMONICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPRAK: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLYCYSTIC KIDNEY DISEASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.7%; Score 55; DB 2; Le
100.0%; Pred. No. 5.1e-15;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                   TOWNSEND and TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                      STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ): NAME/KEY: misc_feature

): LOCATION: 1..246240

): OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-22
Sequence 22, Application US/08724394A
Patent No. 587237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                    ZIE: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KLINGER, KATHERINE W.
APPLICANT: LANDES, GREGORY M.
APPLICANT: BURN, TIMOTHY C.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/08323443B
; Patent No. 5654170
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS: not relevant
not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.C
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: not r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: no
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-323-443B-1
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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RESULT

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTATION UNBER: 31,845
REFERENCE/DOCKET WUMBER: GEN4-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-8415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-658-136-1
; Sequence 1, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-658-136-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 53577 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: ONE MOUNTAIN
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01701
                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ДQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: LANDES, GREGORY M
APPLICANT: CONNORS, TIMOTHY C
APPLICANT: CONNORS, WILLIAM
APPLICANT: GENAINO, GREGORY
APPLICANT: GENAINO, GREGORY
APPLICANT: GIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.5%; Score 48; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.5e-12;
Matches 48; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0372/0A462
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/323,443B FILING DATE: 12-OCT-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
BDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAXIME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFRENCE/DOCKET NUMBER: 0372,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPHONE: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08658136 Patent No. 6071717 GENERAL INFORMATION:
                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 31571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PKD1 GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MASSACHUSETTS: USA
               NUMBER OF SEQUENCES: 8
                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01701
                                                                                                                                                          10022
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                                                                                                                 STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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Query Match 1.5%; Score 48; DB 3; Length 53526; Best Local Similarity 100.0%; Pred. No. 6.3e-12; Matches 48; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: BURN, TIMOTHY C
APPLICANT: BACKONSKI, MILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: GENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENIYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/658,136
REFERENCE DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPAX: 508-872-8400
TELEPAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 51526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Gaps

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                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                             Sequence 105, Application US/08687080
Patent No. 2965427
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
UNMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                             Query Match 1.5%; Score 48; DB 3; Length 53577; Best Local Similarity 100.0%; Pred. No. 6.3e-12; Matches 48; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                         1198 ggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 GCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCACCAGC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE-DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 1318 base pairs
LYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 1.9
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
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Best Local Similarity 100.0'
Matches 47; Conservative
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; INDIVIDUAL ISOLATE:
US-08-687-080-105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
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US-08-687-080-105
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RESULT

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Gaps
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P: 620 Newport Center Drive 16th Floor
Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dougueleret, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAS
FILE REFERENCE: GENSET. 021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/094,121
EARLIER APPLICATION NUMBER: 60/091,563
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
                                                               APPLICANT: Miyai, Kiyoshi
APPLICANT: Naitoh, Tsutomu
APPLICANT: Yonekawa, Toshihiro
TITLE OF INVENTION: Method of Cell Detection
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIKEN1.001APC
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FBASTEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JF95/02734
FILING DATE: 27-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 141, Application US/09247155A
; Patent No. 6312922
; Sequence 2, Application US/08849701; Patent No. 5922544; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: EII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: Alu sequence BLUR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 153 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                           U.S.A.
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-247-155-141/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                             COUNTRY: U.
                                                                                                                                                                                                                                                                          CA
                                                                                                                                                                                                        ADDRESSEE:
STREET: 6
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                                                                                                                                                                                                                                                                          STATE:
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APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
NUMBER OF SEQUENCES: 42
ADDRESSEE: ADDRESS:
ADDRESSEE: MOTGAN & Finnegan
STREET: 345 Park Avenue
CITY: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08367841A

Sequence 12, Application US/08367841A

Sequence 12, Application US/08367841A

Sethert No. 6319674

GENERAL INFORMATION:

APPLICANT: Chader, Gerald J.; Rodriguez,

APPLICANT: Ignacio R.; Mazuruk, Krzysztof;

APPLICANT: Ignacio R.; Mazuruk, Krzysztof;

APPLICANT: Ignacio R.; Mazuruk, Joyce

TITLE OF INVENTION: PIGMENT EPITHELIUM

TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC

TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: 3.3 kb PCR product OTHER INFORMATION: using primers, SEQ ID No. 5840686 15 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.4%; Score 45; DB 2; Length 3267;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 45; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1190 cccaccttggcctcccaaagtgctgggattacaggcatgagccac 1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,963B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07/952,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Morgan & Finnegan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952;
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 12:
SEGUENCE CHARACTERISTICS:
LENGTH: 3267 Base Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: Genomic DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Nucleic Acid
STRANDEDNESS: Double
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown
                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: JT109
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                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                 COUNTRY: US
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                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.4%; Score 45; DB 4; Length 891; Best Local Similarity 100.0%; Pred. No. 1.6e-10; Matches 45; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1033 aacctctgcctcccgggttcaagcgattctcctgcctcagcctcc 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-08-257-963B-12
Squence 12, Application US/08257963B
Patent No. 5840686
GENERAL INFORMATION:
APPLICANT: Patricia; Schwartz, Joan P.;
                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.6999980926514
OTHER INFORMATION: seq LLLFFGKLLVVGG/VG
FEATURE:
LOCATION: 858.863
FEATURE:
          EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 141
LENGTH: 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09078294
Patent No. 6265211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.4%
Best Local Similarity 100.0
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: BAC-F2 contig 5
US-09-078-294-9
                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 4..47
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 4..147
                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: polyA_site
; LOCATION: 880..891
US-09-247-155-141
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LENGTH: 1701
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US-09-078-294-9
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Gaps

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1033 aacctctgcctcccgggttcaagcgattctcctgcctcagcctcc 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 11
LENGTH: 3663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : IDENTIFICATION METHOD:
; OTHER INFORMATION: 3.3 kb PCR product
; OTHER INFORMATION: using primers, SEQ ID No. 6319687 15 and 16
US-08-367-841A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application PC/TUS9507201
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
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1.4%; Score 45; DB 4; Length 3267;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 45; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                           202641260S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morgan & Finnegan, L.L.P.
                                                                                                                                                                                                                                        PRICOR ADDITION: 435
PRICOR ADDITION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-00N-1994
PRICOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REGISTRATION NUMBER: 36434
REGISTRATION NUMBER: 3644
REGISTRATION NUMBER: 3644
REGISTRATION NUMBER: 3644
REGISTRATION NUMBER: 3644
REGISTRATION FOR SEQ ID NO: 12:
SEQUENCE CHARRATERISTICS:
LENGTH: 3567 Bases Pairs
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDENESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WORDPERFECT 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLENCYH: 3267 Basc
TYPE: Nucleic Acid
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MEDIUM TYPE: Floppy 1
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: JT109
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                     COUNTRY:
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Sequence 11, Application US/09499884

Patent No. 6265172

GENERAL INFORMATION:
APPLICANT: St. Clair, Daret
APPLICANT: Urano, Muneyasu
APPLICANT: Urano, Muneyasu
APPLICANT: ASSARSHS, Edward
ITILE OF INVENTION: ASSOCIATED DISEASES
TITLE OF INVENTION: ASSOCIATED DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
OTHER INFORMATION: 3.3 kb PCR product
OTHER INFORMATION: using primers, SEQ ID No: 15 and 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1190 cccaccttggcctcccaaagtgctgggattacaggcatgagccac 1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 45; DB 5; L4 100.0%; Pred. No. 1.5e-10; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                  NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126PCT
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 758-4800
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3267 Base Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 50229-180
CURRENT APPLICATION NUMBER: US/09/499,884
CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06-JUN-1995
                                                                 PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.4%
Best Local Similarity 100.0
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acid
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US-09-499-884-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: Doub
TOPOLOGY: Unknown
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1970 AACCTCTGCCTCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCC 1926

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Length 5581;
                                                                                                                                                                           ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP STREET: 655 Fifteenth St., NW, Suite 300, G St. Lobby
                                                                                              APPLICANT: WEISS, Elisabeth
TITLE OF INVENTION: NEW IMMUNOREGULATORY PROTEIN LST-1
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PATENTIA RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,544
FILING DATE: 18-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
RAPPLICATION NUMBER: PCT EP 96/02663
FILING DATE: 20-JUN-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.4%; Score 45; DB 4; LA
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP 95109511.6
FILING DATE: 20-JUN-1995
APRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112201.9
FILING DATE: 03-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitts, Monica Chin
REGISTRATION NUMBER: 36,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P8341-7073
                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                    Sequence 1, Application US/08973544 Patent No. 6338950 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P83
PELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 638-5000
TELEPAX: (202) 638-4810
INFORMATION FOR SEG ID NO: 1.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 5581 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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2325..2709
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1775..1797
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1475..1567
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LOCATION:
RESULT 15
US-08-973-544-1/c
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US-08-367-841A-43

Sequence 43, Application US/08367841A

Sequence 43, Application US/08367841A

Sequence 43, Application US/08367841A

Setting 10, 6319687

Setting 10, 6319687

APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Tombran-Tink, Joyce
TITLE OF INVENTION: PIGMENT EPITHELIUM

TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
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    Indels
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                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Raftcalails, Rebecca B.
APPLICANT: Wood, Thomas C.
APPLICANT: Wood, Thomas C.
APPLICANT: Otterness, Diane M.
TILLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/18001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT APPLICATION NUMBER: 1998-10-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PastSEQ for Windows Version 3.0
                                      .
0
      0; Mismatches
                                                                                                                                                                                  ; Sequence 37, Application US/09167681A; Patent No. 6265561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (6309)...(6404)
NAME/KEY: CDS
        45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (3730)...(3879)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (3987)...(4112)
NAME/KEY: CDS
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NAME/KEY: CDS
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US-09-167-681-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 37
LENGTH: 8397
                                                                                                                                                  RESULT 16
US-09-167-681-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
        Matches
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COMPUTER READABLE FORM:

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RESULT
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OTHER INFORMATION: full length genomic
OTHER INFORMATION: sequence for PEDF plus flanking sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 43, Application PC/TUS9507201
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Chader, Gerald J.; Becerra, Sofia
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
1.4%; Score 45; DB 4; Length 22481;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 45; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morgan & Finnegan, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA.
APPLICATION NUMBER: PCT/US95/07201
FILLING DATE: 06-UNN-1995
                                                                                                                              FILING DATE: 30-DEC 1994
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NURBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NURBER: 07/952,796
FILING DATE: 24-SED-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6449
INFORMATION FOR SEQ ID NO: 43.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 22481 Base Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Double
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDA.
STREET: 34.
CITY: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: P1-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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PCT-US95-07201-43
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GENERAL INFORMATION:
APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY; TILLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TILLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TILLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: full length genomic OTHER INFORMATION: sequence for PEDF plus flanking sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 84495;
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100.0%; Pred. No. 1.3e-10;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 17174 CCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC 17218
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CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEO ID NOS: 5
SOFTWARE: FastSEO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                        20264126PCT
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  ATTORNET/AGENT INFOLENTIAL
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 758-4800
TELEFAX: (212) 758-4800
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3, Application US/09797906
; Patent No. 6329188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; LOCATION: (1)...(84495)
; OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
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US-08-724-394A-22

Sequence 22, Application US/08724394A

Patent No. 587237

GENERAL INFORMATION:

APPLICANT: Reder, John N.

APPLICANT: Kronmal, Gregory S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECULARY: 246240 ~--
TYPE: nucleic acid
STRANDEDNESS: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
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                                                                                                                                                                        APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
CORRESPONDENCE 31
CORRESPONDENCE ADDRESS:
ADDRESSE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: O1-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGBMT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 415-576-0200
TELEFRAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature

!COCATION: 1..246240

| OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDIUFER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-724-394A-21; Sequence 21, Application US/08724394A; Pattent No. 5872237; Pattent No. SRATEAL INFORMATION:
                Sequence 20, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
                                                                                      Feder, John N.
Kronmal, Gregory S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                 Lauer, Peter M.
Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
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US-08-724-394A-20
                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                              CITY: STATE:
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Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: TWO Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTR: CA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SPETIAND APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-02T-1996
CLASSIFICATION NUMBER: 05-02-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,136
REFERENCE/COCKET NUMBER: 017957-000100
TELEPHONE: 415-576-0300
INFORMATION FOR SED ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21
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Gaps

COMPUTER READABLE FORM:

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Length 2310;
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
Db 45158 CCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGC 45115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: TEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-JUN-1995
CLASSIPICATION: 435
                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: IGARASHI, KOICHI
APPLICANT: SENOO, Masaharu
APPLICANT: WATANABE, Tatesuy
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
1.3%; Score 43; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 43; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION 479.

APPLICATION NUMBER: US/08/149,664
FILING DATE: 16-AUG-1991
APPLICATION NUMBER: US 07/743369
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINEK, ETHOST W
REGISTRATION NUMBER: 29822
                                                                                                                            ; Sequence 9, Application US/08471570 ; Patent No. 5750371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-471-570-7/c
; Sequence 7, Application US/08471570
; Patent No. 5750371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: IGARASHI, KOİCHİ
APPLICANT: SENOO, Masaharu
APPLICANT: WATANABE, TATSUYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617)523-6440
TELEFX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 130 Water Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 2310 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Massachusetts
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                                                                                                      US-08-471-570-9/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION:
US-08-471-570-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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Fatent No. 617764
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
TITLE OF ILLUG DATE: 1998-08-03
CURRENT FILLING DATE: 1998-08-03
FARLIER PILLING DATE: 1998-07-02
EARLIER PILLING DATE: 1998-07-02
EARLIER FILLING DATE: 1998-07-03
FARLIER FILLING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 18
SOFTHANE: FRALER FILLING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
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1.4%; Score 44; DB 3; Length 176373;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 44; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oy 1194 ccttggcctcccaaagtgctgggattacaggcatgagccatgc 1237
                                                                        OPERATION SYSTEM: PC-LUDS/MS-LUDS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTONEX/AGENT INFORMATION:
NAME: FILLS, Renee A.
REGISCHARTION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 35,136
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: A 15-576-0200
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHRARACTERISTICS:
LENGTH: 246240 base pairs
TENGTH: APPLICATION INFORMATION:
TENGTH: CARRACTERISTICS:
TENGTH: CARRACTERISTICS:
TENGTH: A 15-576-0304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22
             MEDIUM TYPE: Floppy disk
Computer: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)....(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS: not relevant not relevant
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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US-09-128-155-17/c
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TOPOLOGY:
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US-09-496-694B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2676;
                                                   ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Fatentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-00N-1995
CIASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/149,664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Le
1.1e-09;
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.3%; Score 43; DB Best Local Similarity 100.0%; Pred. No. 1.1.
Matches 43; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               US 07/743369
                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 35, Application US/08975080 Patent No. 6245523 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 40:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (61)757-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2676 base pairs
TYPE: nucleic acid
STRANDEDRESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29822
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: US 07
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: LINEK, Ernest V
REGISTRATION NUMBER: 2
                                                                                                                CITY: Boston
STATE: Massachusetts
                  NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. CONSERT
TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
FILE REPERBNCE: RTS-0053
CURRENT APPLICATION NUMBER: US/09/630,706
CURRENT FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 94
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1035 cctctgcctcccgggttcaagcgattctcctgcctcagcctcc 1077
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INCORATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.3%; Score 43; DB 4; Le Best Local Similarity 100.0%; Pred. No. 1e-09; Matches 43; Conservative 0; Mismatches 0;
                                                                                                                                                                                         NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 10, Application US/09630706
; Patent No. 6277640
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) US-08-975-080-35
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 14796 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY: CDS
LOCATION: (11955)...(12044)
US-09-630-706-10
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NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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LOCATION: (28)
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Sequence 7, Application US/09268992
Patent No. 6342351
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                          GENERAL INFORMATION:
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LENGTH: 72604
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                                                                  APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Eric E. Swayze
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REPERENCE: ISPH-0439
CURRENT APPLICATION NUMBER: US/09/496,694B
CURRENT FILING DATE: 1090-0-2-02
PRIOR APPLICATION NUMBER: 09/286,407
PRIOR PILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 249
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Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 43; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 43; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Mollenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REPERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
BARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
Sequence 3, Application US/09496694B Patent No. 6335194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09341587
Patent No. 6346606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (5158)...(5275)
NAME/KEY: CDS
; LOCATION: (11955)...(12044)
US-09-496-694B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (2811)...(2921)
NAME/KEY: CDS
LOCATION: (3174)...(3283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
US-09-341-587-7
                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 14796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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Gaps
APPLICANT: Chen, H.
APPLICANT: Freimer, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18P RELATED DISORDERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08812204
Patent No. 5965790
GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
TITLE OF INVENTION: THERAPEUTIC METHODS OF USE
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.3%; Score 43; DB 4; Lo Best Local Similarity 100.0%; Pred. No. 9.6e-10; Matches 43; Conservative 0; Mismatches 0;
                                                                                  CURRENT APPLICATION NUMBER: US/09/268,992
CURRENT FILING DATE: 1999-03-16
EARLIER APPLICATION NUMBER: 09/236,134
EARLIER FILING DATE: 1999-01-22
EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: 60/106,056
EARLIER APPLICATION NUMBER: 60/068,312
EARLIER FILING DATE: 1998-10-28
EARLIER FILING DATE: 1998-06-05
EARLIER FILING DATE: 1998-06-05
EARLIER FILING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 84
SOFTHARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIA-014.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEPRAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: all n positions
; OTHER INFORMATION: n=a, c, g, or t
US-09-268-992-7
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COUNTRY: U.S.A.
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                               US-08-465-981-2
                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                          CITY:
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100.0%; Pred. No. 3.2e-09;
tive 0; Mismatches 0; Indels
                                                                                                                                                                          Length 1613;
                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                         1040 gcctcccgggttcaagcgattctcctgcctcagcctcctgag 1081
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Kufe, Donald
APPLICANT: Abe, Miyako
APPLICANT: Abe, Miyako
TITLE OF INVENTION: GENE TRANSCRIPTION AND
TITLE OF INVENTION: IONIZING RADIATION: METHODS
TITLE OF INVENTION: AND COMPOSITIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                          Query Match
1.3%; Score 42; DB 2; Lu
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 42; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/065001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/999,742
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08324465
Patent No. 5565334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Fish & Richardson 225 Franklin Street
                                                                            TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-812-204-1
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SEQUENCE CHARACTERISTICS:
LENGTH: 1613 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 02110-2804
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US-08-324-465-2
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GENERAL INFORMATION:
APPLICANT: Kufe, Donald
APPLICANT: Abe, Miyako
TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING
TITLE OF INVENTION: EXPRESSION IN EPITHELIAL CELLS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                   GENERAL INFORMATION:
APPLICANT: Kufe, Donald
APPLICANT: Abe, Miyako
TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING
TITLE OF INVENTION: EXPRESSION IN EPITHELIAL CELLS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.3%; Score 42; DB 2; L6
100.0%; Pred. No. 3.2e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                ZIP: 02110-2804
COMPOTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA: 00.000
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/465,981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIASSIFICATION: 435
PRIOR APPLICATION DATA: 08/324,465
FILING DATE: October 17, 1994
APPLICATION NUMBER: 07/999,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
; Sequence 2, Application US/08465981
; Patent No. 5874415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (617) 542-5070 (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 1.34
Best Local Similarity 100.0
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fraser, Janis K. REGISTRATION NUMBER: 3
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 02110-2804
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                                                                                                                                                                                                                          Boston
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Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 42; Conservative 0; Mismatches 0; Indels
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Fatent No. 556334
GENERAL INFORMATION:
APPLICANT: Rufe, Donald
APPLICANT: Abe, Miyako
TITLE OF INVENTION: GENE TRANSCRIPTION AND
TITLE OF INVENTION: IONIZING RADIATION:
TITLE OF INVENTION: AND COMPOSITIONS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11915
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPPRATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                          NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/065WO1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPACE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/065001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/999,742
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                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/999,742
FILING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US,
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
PCT-US93-11915-2
                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 225 Fr
CITY: Boston
STATE: Massach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1656
                                                                                                                                                                                  FILING DATE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Kide, Donald
APPLICANT: Abe, Miyako
TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING
TITLE OF INVENTION: ENPRESSION IN EPITHELIAL CELLS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                               1040 gcctcccgggttcaagcgattctcctgcctcagcctcctgag 1081
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/324,465
FILING DATE: October 17, 1994
APPLICATION NUMBER: 07/999,742
FILING DATE: December 31, 1992
ATTORNEY AGENT INFORMATION:
NAME: Fraser, Janis K.
RECISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/065002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617),542-5770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WORDPETECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-465-981-5
Sequence 5, Application US/08465981
Patent No. 5874415
TELECOMMUNICATION INFORMATION:
                   TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELES: 200154
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (617) 542-8906
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                                                                                                                                                          nucleic acid
EDNESS: double
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: double
                                                                                                                                                                                                          ; TOPOLOGY: linear
US-08-324-465-5
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US-08-465-981-5
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ZIP: 02110-2804
                                                                                                                                                                                STRANDEDNESS:
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D.C.
USA
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LENGTH: 5590
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                                  COUNTRY:
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                                                                                                                                                             Sequence 5, Application PC/TUS9311915
GENERAL INFORMATION:
APPLICANT: Kufe, Donald
APPLICANT: Kufe, Myako
TITLE OF INVENTION: ENPRESSION IN EPITHELIAL CELLS
NUMBER OF SEQUENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1040 gcctcccgggttcaagcgattctcctgcctcagcctcctgag 1081
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US-08-655-640-5
; Sequence 5, Application US/08655640
; Patent No. 5948613
; GENERAL INFORMATION:
; APPLICANT: Teng, Christina
; APPLICANT: Panella, Timothy J.
; TITLE OF INVENTION: HUMAN LACTOFERRIN
; TUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVE. N.W., NINTH FLOOR
; CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3%; Score 42; DB 5; L
100.0%; Pred. No. 3.1e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/065W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPRAN: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/999,742
FILLING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
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TELEX: 200154
INFORMATION FOR SEQ INO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double
                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                         Boston
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PCT-US93-11915-5
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; Sequence 129, Application US/09050159A
; Patent No. 6137505
; GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: No. 6197505berg, Leif T
APPLICANT: Linstrom, Par H
; APPLICANT: Linstrom, Par H
; TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND
; TITLE OF INVENTION: COMPOSITIONS FOR USF THEREOF
; TITLE OF INVENTION: US/09/050,159A
; CURRENT APPLICATION NUMBER: US/09/050,159A
; CURRENT FILING DATE: 1998-03-27
; EARLIER PRILING DATE: 1987-04-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver: 2.1
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Best Local Similarity 100.0%; Pred. No. 3e-09;
Matches 42; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.3%; Score 42; DB 2; Length 208 Best Local Similarity 100.0%; Pred. No. 3.1e-09; Matches 42; Conservative 0; Mismatches 0; Indels
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                                                                                                                        OURTHAING SYSTEM: RC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,640
FILING DATE: 30-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/992,538
FILING DATE: December 17, 1992
ATTORNEY/AGENT INFORMATION:
NAMME: SCOTY, WATSON T.
REGISTRENCE/DOCKET NUMBER: WTS/5683/98019/SAP
TELECOMMUNICATION NUMBER: WTS/5683/98019/SAP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (202) 861-3000
TELEFA: (202) 822-0944
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CRARACTERISTICS:
LENGTH: 2086 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1195 cttggcctcccaaagtgctgggattacaggcatgagccactg 1236
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                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
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20005-3918
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COUNTRY:
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                                                                                                                                                                         APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: RASER, PAUL B
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHELMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
1837 ctctgcctcccgggttcaagcgattctcctgcctcagcctcc 1878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 CTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC 52
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1.3%; Score 41; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                    STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                      TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               Sequence 107, Application US/08967101
Patent No. 5840540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 107, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7100 TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 107: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (genomic)
US-08-967-101-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 198 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                     Massachusetts: U.S.A.
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MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                              02110
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                                                                                        US-08-967-101-107
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                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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Patent No. 6117978
GENERAL INFORMATION:
APPLICANT: ST. GENGRE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 198;
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                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.3%; Score 41; DB 2; Ls
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 41; Conservative 0; Mismatches 0;
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STREET: High Street Tower - 125 High Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                          NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (genomic)
US-08-592-541-107
                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SED ID NO: 107
SEQUENCE CHARACTERISTICS:
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TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 107
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 198 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 base pairs
                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CLASSIFICATION: 800
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                                                                                                               OPERATING SYSTEM:
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U.S.A.
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-124-698-107
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Patent No. 6210919
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                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OP SEQUENCES: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.3%; Score 41; DB 4; Length 198; Best Local Similarity 100.0%; Pred. No. 9.6e-09; Matches 41; Conservative 0; Mismatches 0; Indels
                                                                                                                                              Query Match
1.3%; Score 41; DB 3; Length 198;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 41; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1194 ccttggcctcccaaagtgctgggattacaggcatgagccac 1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/127,480
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-496-841C-107; Sequence 107, Application US/08496841C
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                            Sequence 107, Application US/09127480 Patent No. 6194153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: PICCHE, Edmund R.
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic) US-09-127-480-107
                                                      MOLECULE TYPE: DNA (genomic) US-09-124-698-107
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TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Massachusetts
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MEDIUM TYPE: Floppy of
          TYPE: nucleic acid
STRANDEDNESS: single
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                            STRANDEDNESS:
TOPOLOGY: lin
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                                                                        FRASER, PAUL E
FITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
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GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRAMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.3%; Score 41; DB 4; Length 198; 100.0%; Pred. No. 9.6e-09;
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PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
FLING DATE: 28-Jun-1995
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.3%; Score 41; DB Best Local Similarity 100.0%; Pred. No. 9.6 Matches 41; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic); SEQUENCE DESCRIPTION: SEQ ID NO: 107: US-08-496-841C-107
GENERAL INFORMATION:
GENERAL INFORMATION:
ROMMENS, JOHANNA M
FRASER, PAUL E
FRASER, CHOULES
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ADDRESSEE: TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                            NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
REGISTRATION NUMBER: 35,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
ELEFEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 103, Application US/08967101 Patent No. 5840540
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                            STATE: New York
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10.NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
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0; Gaps Query Match
1.3%; Score 41; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 9.3e-09;
Matches 41; Conservative 0; Mismatches 0; Indels

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Search completed: September 20, 2002, 06:14:47 Job time: 11106 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

September 20, 2002, 00:17:46; Search time 3900.56 Seconds (without alignments) 11180.103 Million cell updates/sec Run on:

Title:

US-09-846-456-1 3231 1 acagggcatggtggcaggtg......gccccacatccccacct 3231 Perfect score:

Scoring table: Sequence:

13736207 seqs, 6748477542 residues OLIGO\_NUC Gapop 60.0 , Gapext 60.0 Searched:

0 Word size :

Total number of hits satisfying chosen parameters:

27472414

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

EST:\* Database :

gb\_est2:\*
gb\_htc:\*
gb\_gss:\*
em\_gss\_hum:\*
em\_gss\_inv:\*
em\_gss\_inv:\*
em\_gss\_inv:\* em\_estba:\*
em\_esthum:\*
em\_esthum:\*
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em\_estpl:\* 10: 111: 12: 13: 14: 16:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No.   Score Match Length DB   ID	Description	AU121731 AU121731	AU135588 AU135588	Z44377 HSC1ZB081 n	AW748338 RC6-BT025	AA527406 ng37c02.s	BG678861 602624760	BE178833 PM0-HT060	AQ538994 RPCI-11-3	AA652813 ns74c05.s	AG067644 Pan trogl			BG745912 602724092	BG014649 IL5-GN023	BG007260 IL5-GN023	AQ056873 CIT-HSP-2	AA010265 zi09e05.s
Score 1154 1154 1116 1111 1116 1116 1116 1116	ΙD	AU121731	AU135588	244377	AW748338	AA527406	BG678861	BE178833	AQ538994	AA652813	AG067644	BI059823	BI015195	BG745912	BG014649	BG007260	AQ056873	AA010265
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Score 1154 1154 1116 1111 1116 1116 1116 1116	Length	763	736	292	289	467	866	617	219	424	674	269	009	1054	384	387	444	325
	Query Match	10.4	6.7	4.8	3.9	3.4	3.0	1.8	1.8	1.8	1.8	1.7	1.7	1.7	1.7	1.7	1.7	1.7
Result No. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Score	336	217	154	126	111	86	28	57	57	57	56	26	56	55	55	55	54
	ult No.	; ;	~	٣	4	Ŋ	φ	7	œ	0	10	11	12	13	14	15	16	17
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	AQ48571 RPCI-11-2 AW971724 EST383813 AQ62366 HS_5319_A AIO84593 Ox63f01.s AQ589333 CTRBI-E1- AV718287 AV718287 AQ10874 RPCII1-59 AA662976 AC52b01.s H90008 yua33403.s.1 AA486970 Ab17f12.r BF924753 CMI-NT020 AQ280600 CITBI-EI-
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0 0 0 118	0000 000 0000 000 0000 000

## ALIGNMENTS

763 bp mRNA linear EST 19-OCT-2000 MAMMA1 Homo sapiens cDNA clone MAMMA1000851 5', mRNA 1 GI:10936966	human. Homo sapiens Homo sapien	Isogai, T. HRI human cDNA project Unpublished (2000) Contact: Takao Isogai Genomics Laboratory Genomics Laboratory 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 181-488-52-3951 EMA: 181-438-52-3952 EMA: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute, con library construction: Department of Pirology, Institute of Medical Science, University of Tokyo, and	earch Institute. Location/Qualifiers L. 763 Aorganism="Homo sapiens" Aclone="MaxMA100881" Aclone="MaMMA100881" Aclone=lib="MaMMA1" Aclone=lip="mamMA1" Aclone=lip="mamMA1" Aclone=lip="mamMA1" Aclone=lip="mamMA1"	205 c 260 g 158 t 3 others
AU121731 AU121731 MAMMA1 sequence. AU121731 AU121731.1 GI:1 EST.	human.  Homo sapiens  Eukaryota; Metazoa;  Mammalia; Eutheria;  I bases 1 to 763)  Ota,T., Nishikawa,T.  Yamamoto,J., Wakamat	Isogai, T.  HRI human CDNA project Unpublished (2000) Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Cl Tel: 81-438-52-3951 Fax: 81-438-52-3952 Email: genomics@hri.co.jj HRI human CDNA project; Research Institute; CDNA Virology, Institute of MA	Helix Research Institute. Location/Qualifi 1763 /organism="Homo /db_xref="taxon: /clone="MAMMA100"/ /tissue_type="mamana"/	137 a 200
RESULT 1 AU121731 LOCUS DEFINITION ACCESSION VERSTON KEYWORDS	N H S	TITLE JOORNAL COMMENT	FEATURES SOUTCE	BASE COUNT ORIGIN

Gaps

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0; Indels

Mismatches

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Matches 217; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                2956 gggctgcggcagggcagggcgggagctccgcgcaccaacagagccggttctcagggcgc 3015
                                                                                                                                                                                                                                         2896 aattgcgagcgagagtgagtgggccgggacccgcagagccgagccgaccttctccc 2955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases I to 736)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                         1 AATTGCGAGCGAGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCTTCTCTCCC 60
                                       0; Gaps
   Ouery Match 10.4%; Score 336; DB 9; Length 763; Best Local Similarity 100.0%; Pred. No. 1.9e-126; Matches 336; Conservative 0; Mismatches 0; Indels
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
THEL: 81-438-55-3951
Fax: 81-438-52-3952
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AU135588.1 GI:10996127
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Contact: Takao Isogai
Genomics Laboratory
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JOURNAL
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KEYWORDS
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Length 736;

DB 9;

6.7%; Score 217; DB 9; 1 100.0%; Pred. No. 6.9e-78;

Query Match Best Local Similarity

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/tissue_type="total brain"
/tissue_type="total brain"
/dev_stage="3 months old"
/forte="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex-Female; dev_stage=3 months old;
Site_2: NotI; sex-Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
50 a 87 c 96 g 56 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 14-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 292)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
HSC1ZB081 normalized infant brain cDNA Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-lzb08
Seq primer: ('21)M13_universal.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genexpress Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995) 95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="c-1zb08"
/clone_lib="normalized infant brain cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 154; DB 10;
Pred. No. 5.7e-52;
                                                                                                                                                                                                                                                                                                 3078 taggagaaagagacgcaaacacaaaagtggaaaacag 3114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRNA
                                                                                                                                                                                                                                                                                                                                185 TAGGAGAAAGAGACGCAAACACAAAAAGTGGAAAACAG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.8%;
99.5%;
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Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .292
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Best Local Similarity
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/note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-BT0252-271099-012-c10&t3=1999-10-27&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW748338 1252-271099-012-c10 BT0252 Homo sapiens cDNA, mRNA sequence.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \operatorname{Simpson}, \operatorname{A.J.} Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                       2910 gtgagtggggcgggacccgcagagccgacctcactctctcccgggctgcggcaggg 2969
                                                                                                                                                                                                                                                                                                                                                                                                                                  3030 tttccccggttctgttttctccccttctccggaaggcttgtcaaggggtaggagaaagag 3089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCCCCGGGCTGCGGCAGGG 60
    0; Gaps
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        1; Indels
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        0; Mismatches
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/db_xref="taxon:9606"
/clone_lib="BT0252"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence start: 146
High quality sequence stop: 289.
Location/Qualifiers
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Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3090 acgcaaacacaaaagtggaaaacag 3114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ACGCAAACACAAAAGTGGAAAACAG 205
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        Matches 204; Conservative
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DEFINITION
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AW748338/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NII-GAP clone distribution: NII-GAP clone distribution on through the I.M.A.G.E. Consortium/LLNL at: www-bio.lnl.igov/bbrp/image/image.html
Insert Length: 1057 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                     AAS27406 467 bp mRNA linear EST 21-AUG-1997 ag37c02.sl NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:936962 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCICGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                    2006 gotgoacttcacaaatgtatacaaactaaatacaagtcotgtgtttttatcacagggagg 2065
                                                                                                                                                                   Gaps
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Length 289;
                                            0; Indels
3.9%; Score 126; DB 9; I
100.0%; Pred. No. 1.5e-40;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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/clone_lib="NCI_CGAP_Co3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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1. .467
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100.0%; Pic
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Best Local Similarity 100.0
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
                                                Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
AA527406
        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                              2126 ttgttt 2131
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AA527406
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2152 tttgtggcctccttcctctcaatttatgaagaagaagcagtaagatgttcctctcgggtcc 2211

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ORIGIN

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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone_lib="Huf0608"
/dev_stage="Adult"
/dote="Organ: head_neck; Vector: pucl8; Site_l: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
14 a 128 c 150 g 145 t
                                                     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal, M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costo,F.F., Garvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2-PMO-HT0608-170 300-001-f02&t3=2000-03-17&t4=1)
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RPCI-11-343L18.TJ RPCI-11 HOMO Sapiens genomic clone RPCI-11-343L18
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                      Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
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                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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High quality sequence start: 14
High quality sequence stop: 612.
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Other_GSSs: RPCI-11-343L18.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ538994.1 GI:4869633
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                                                                                                                                                                                                              Simpson, A.J.
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Best Local Similarity
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                                                                                                                                                                                                                                                                    602624760F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4749735 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyt Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMN0603 row: g column: 16
High quality sequence stop: 860.
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/clone=lib="NCL_CGAP_Skn4"
/tissue_trpe="Squamous cell carcinoma"
/tab_bost="Squamous cell carcinoma"
/lab_bost="Organ: Skin: Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."

233 c 244 g 236 t
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
0; Gaps
                                                                    2212 totgagggacotggggagotcaggctgggaatotocaaggcagtaggtcgc 2262
                                                                                                   Length 998;
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100.0%; Pred. No. 2.2
Live 0; Mismatches
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                  998 pb
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BG678861
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FEATURES

BASE COUNT

ORIGIN

Matches

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LOCUS

ACCESSION

VERSION

KEYWORDS

SOURCE

BE178833/c

RESULT

ORGANISM

TITLE

COMMENT

REFERENCE AUTHORS

RESULT BG678861

ò q ACCESSION VERSION KEYWORDS

SOURCE

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Gaps

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Tissue Procurement: W. Marston Li.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA652813 424 bp mRNA linear EST 17-MAR-1999 ns74c05.sl NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1189352 similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                         Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
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Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.B. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 560 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                 9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
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Location/Qualifiers
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="RPCI-11-343118"
/clone_lib="RPCI-11"
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Best Local Similarity 100.0
Matches 57; Conservative
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/organism="Homo sapiens" /db\_xref="taxon:9606"

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Bubmitted (O2-MGG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbes@geor.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tpl:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG067644.1 GI:16619446
AG067644.1 GI:16619446
GSS; GSS (genome survey sequence).
GSS; GSS (genome survey sequence).
Fan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-057L02.R.
Pan troglodytes
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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BAC end sequences of Library PTB
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/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 57; DB 9; Length 424; 100.0%; Pred. No. 1.8e-12;
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/db_xref="taxon:9598"
/clone="PTB-057L02.R"
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/clone="IMAGE:1189352"
/clone_lib="NCI_CGAP_Pr2"
/sex="Male"
                                                                        /dev_stage="45 years old"
/lab_host="DH10B"
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R.Site 2 : SacT
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Query Match

Matches

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RESULT 1: BI059823

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AUTHORS

JOURNAL MEDLINE

COMMENT

TITLE

BASE COUNT

EST 13-JUN-2001

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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deolivelra, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-ET0140-
190201-006-ell2&t3=2001-02-19&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 72.
                                                                                                                                                          BI015195 600 bp mRNA linear EST 13-JUN-200:
MR4-ET0140-190201-006-e12 ET0140 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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602724092T1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4850375 3',
mRNA sequence.
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EST.
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Laboratory of Gancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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/organism="Homo sapiens"
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/clone_lib="ET0140"
/dev_stage="Adult"
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., Garchin, S., Coste, F.F., Galdman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'flare, M.J., Soares, F., Brehtani, R.R., Reis, L.F., de Souza, S.J. and
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LL1-UT0115-080101-378-H06 UT0115 Homo sapiens cDNA, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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tive 0; Mismatches 0; Indels
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="lipf0115"
/dev_stage="Adult"
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179
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/lab_host="DHIOR (phage-resistant)"
/lab_host="DHIOR (phage-resistant)"
/note="Corgan: spleen; Vector: porB7; Site_1: XhoI; Site_2:
/note="Corgan: spleen; Vector: porB7; Site_1: Zite_2: Corgan: spleen; Vector: porB7; Site_1: Zite_2: Corgan: spleen; Vector: porB7; Site_1: Zite_2: Corgan: spleen; Vector: porgan: properties of the corganization of the corganization of the corganization of Carlifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II R (Life Technologies). Note: this is a lange of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization of the corganization 
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.ih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
hcolumn: 24
High quality sequence stop: 841.
Location/Qualifiers
                                                                                                                                            1 (bases 1 to 1054)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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100.0%; Pred. No. 2.9e-12;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:4850375"
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/clone_lib="GAOUST"
/dev_stage="Adult"
/dev_stage="Adult"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Ourgan: placenta_normal; Vector: puc18; Site_1: SmaI
/Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
Research) profiles into the pUC 18 vector. Reverse
performed under low stringency conditions."
a 110 c 87 g 100 t lothers
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LL5-GN0239-271100-281-e06 GN0239 Homo sapiens CDNA, mRNA sequence.
BG007260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Cafolman, G.H., Carvalho, A.F., Matsukma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-GN0239-
271100-281-eo6&t3=2000-11-27&t4=1)
Seq primer: puc 18 forward
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Fax: +55-11-2704922
Fax: +55-11-2707001
Bmail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=LIS&t2=IL5-GN0239-21120-342-907&t3=2000-12-21&t4=1)
Seq primer: puc IB forward
High quality sequence stop: 360.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 387)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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Gaps

Indels

EST 09-MAY-1997

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Dukaryotz, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 325)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, M., Hawkins, M., Fullman, M., Kucaba, T., Legy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTyT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Patima Bonaldo."
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325 bp mRNA linear EST 09-MAY-19
Z109e0.53 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA
clone IMAGE:430304 3' similar to contains Alu repetitive element
contains element MER22 repetitive element i, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1517 Std Error: 0.00
Seq primer: mob.REGA+FT
High quality sequence stop: 274.
                                                                               1190 cccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 1244
                                                                                                          157 CCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:430304"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.7%; Score 54; DB 9; Length 325; 100.0%; Pred. No. 3.5e-11; tive 0; Mismatches 0; Indels
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            100.0%; Pred. No. 1.2e-11; ive 0; Mismatches 0;
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/db_xref="GDB:1330073"
/db_xref="taxon:9606"
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AA010265.1 GI:1471442
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                                  55; Conservative
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Matches 54; Conservative
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            Similarity
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                                  Matches
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                                                                                                                                                                                                                       AA010265
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                                                                                                                                                                                                                                                                                                                                                                    VERSION
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                                                                                                                                     /note="Organ: placenta_normal; Vector: pucl8; Site_1: Smal Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 1 (basea I to 444)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS 30-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIT-HSP-2339H7.TF CIT-HSP Homo sapiens genomic clone 2339H7, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1190 cccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 CCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGGGCCCAGC 183
                                                                                                                                                                                                                                                                                                                                                                                                         Length 387;
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Contact: Mark Adms
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                  1.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.7%; Score 55; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.2e-11
Matches 55; Conservative 0; Mismatches 0
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                                            /organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                  /db_xref="taxon:9606"
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Unpublished (1998)
Other_GSSs: CIT-HSP-2339H7.TR
  Location/Qualifiers
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/sex="Male"
                                                                                           /clone_lib="GN0239"
/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mdadams@tiqr.org
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Class: BAC ends.
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FEATURES
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DEFINITION

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KEYWORDS

SOURCE

ORGANISM

AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

REFERENCE

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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausled by Contact Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Parayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lln.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 424.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /ncte="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 468)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov.e. column: 06
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCI_CGAP_Ov23"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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BG576148
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 405)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -4UUP from Glbco
High quality sequence stop: 385.
                                                                                                                                                             BF431825
nab50h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3269606 3' similar to contains Alu repetitive element :contains element MER22 repetitive element; mRNA sequence.
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                  194 CCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAG 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 54; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone-"IMAGE:3269606"
                                                                                                                                                                                                                                                                                                                    BF431825.1 GI:11443939
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Unpublished (1997)
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BASE COUNT ORIGIN

DEFINITION

AW104031

LOCUS

RESULT

ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

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0; Gaps

Indels

Gaps

; 0

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A1610607 658 bp mRNA linear EST 13-MAY-1999 tpl9909.xl NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188288 3' similar to TR:Q99634 Q99634 RIG-G. [1] ; contains Alu repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/bbrp/image/image.html
Insert Length: 2270 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: stomach; vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 658)

NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                  1189 gcccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgccc 1241
                                                                                                          Length 658;
                                           Indels
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              Pred. No. 7.5e-11; 
; Mismatches 0;
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1.6%; Score 53; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 6.2e-11;
Matches 53; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:2188288"
/clone_lib="NCI_CGAP_Gas4"
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100.08; Pie
                                                                                                                                                                                                                                                                                                                    element;, mRNA sequence.
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BI062371.1 GI:14469898
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AI610607.1 GI:4619774
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Unpublished (1997)
                                         53; Conservative
                     Best Local Similarity
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                                                                                                                                                                                                                      A1610607
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 23-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ663862 453 bp DNA linear GSS 23-JUN-1999
HS_2151_B1_G10_T7C CIT Approved Human Genomic Sperm Library D Homo
saptens genomic clone Plate=2151 Col=19 Row=N, DNA sequence.
                                                                                                                                                                                       /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High Throughput Sequencing Center University of Washington University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Eax: (206) 616-3887 Exi: (206) 616-3887 Enail: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="Plate=2151 Col=19 Row=N"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                              /clone="IMAGE:4705901"
/clone_11b=NIH_MAC_87"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.7%; Score 54; DB 10; Length 814; Best Local Similarity 100.0%; Pred. No. 2.2e-11; Matches 54; Conservative 0; Mismatches 0; Indels
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Plate: 2151 row: N column: 19
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                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0117-
160301-502-EL0_18f3=2001-03-16&t4=1)
Seq Primer: puc 18 forward
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1 (bases 1 to 249)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 233)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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tive 0; Mismatches 0;
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Location/Qualifiers
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                                                                                                          Homo sapiens
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XhOI; Site_2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer; in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol:shtml).
please contact Hiroshi Inoue, MD/Phb for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

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1 (Daess I to 340)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistan, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, Schmitt, A., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y., and Bowers, Y.
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                                                                                                                                                                                                                                                                                                                                                  Library was constructed by Dr. J. Ferrer In vivo mass-excised to paluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Seq primer: -40RP from Gibco High quality sequence stop: 190.

Location/Qualiflers
                                                                                  Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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/note="Organ: pancreas: Vector: pBluescript SK-; Site_l:
/stratgene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
/iniversity protocol
/(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hirosh! Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 SEuclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library. "
                                                                                                                                                                                         Library was constructed by Dr. J. Ferrer In vivo mass-excised to Balescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For Information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Sossbble reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco High quality sequence stop: 316.
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gi08h11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1855941
3' similar to contains Alu repetitive element;, mRNA sequence.
A1264119
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                  Endocrine Pańcreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 391)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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/db_xref="taxon:9606"
                                                                                                                                                                      dmelton@biohp.harvard.edu
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Matches 52; Conservative
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(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: ECO RI: Equal amounts of plasmid DNA_from three
normalized libraries (melanocyte 2NbHW, pregnant uterus
NBHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
34048B-345479, and 48448B-489479."
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrpy/lange/image.html
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA481408 to CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746368 3' similar to contains Alu repetitive element; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

M. (bases 1 to 414)

NCI-CGAP http://www.nobi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
/clone_lib="Soares_NiHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.0
Watches 52; Conservative
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1074 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 400.
Location/Qualifiers
primed with a Not I - ollgo(dT) primer [CBER]. cDNA synthesis was primed with a Not I - ollgo(dT) primer [C - regrate/CRACTGGGAGCGGCCCCCTATTTTTTTTTTTTTT-3' [S - regrated contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 416)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Onpubblished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1679442 Homo sapiens cDNA clone IMAGE:2255773 3/
similar to contains Alu repetitive element; contains element TAR1
repetitive element; , mRNA sequence.
A1679442 GI:4889624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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100.0%; Pred. No. 2e-10;
tive 0; Mismatches 0; Indels
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/clone_lib="NCI_CGAP_Gas4"
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VERSION
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
www-bio.lln.gov/bbrp/image/image.html
Insert Length: 528 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="Indexcoll:9000"
/clone="Indexcoll:9000"
/clone="Indexcoll:9000"
/clone="Indexcoll:9000"
/tissue_type="pooled germ cell tumors"
/lab_host="Dooled germ cell tumors"
/lab_host="Dooled germ cell tumors"
/lab_host="Dooled germ cell tumors"
/lab_host="Dooled germ cell tumors"
/note="Vector: pT73D-pac (Pharmacia) with a modified
/note="Vector: pT73D-pac (Pharmacia) with a modified
/note="Vector: pT73D-pac (Pharmacia) with a modified
/note="Vector: pT73D-pac (Pharmacia) NA
from the normalized library NCI_CGAP_GC4 was prepared,
and
from the normalized library NCI_CGAP_GC4 was prepared,
and
from the normalized library NCI_CGAP_GC4 was prepared,
and
from the normalized library nciloration,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 417)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                            AI337065 417 bp mRNA linear EST 15-FEB-1' gx82g11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2009060 3' similar to contains Alu repetitive element;, mRNA sequence.
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Length 417;
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Best Local Similarity 100.0%; Fred. No. 2e-
Matches 52; Conservative 0; Mismatches
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VERSION

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Gaps

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1.6%; Score 52; DB 9; Length 416; 100.0%; Pred. No. 2e-10; tive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 52; Conservative

Query Match

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Email: asimpsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=Li3st2=IL3-UF0117-
160301-502-G10st3-2001-03-16st4=1)
Seq primer: puc 18 forward
High quality sequence stop: 450.
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 01-0CT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIO89524 455 bp mRNA linear EST 01-0CT-1996 oz22a01.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676040 3' similar to contains Alu repetitive element; , mRNA
                     Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 761 Std Error: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 444.
Location/Qualifiers
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/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="#8-9 weeks"
/lab_host="pH108"
                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
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/dev_stage="Adult"
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                                                                    Tel: +55-11-2704922
                                                                                              Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52; Conservative
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DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
the Chound through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/Dbrp/image/image.html
Seq primer: -400P from Gibco
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1 (bases 1 to 450)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Brunsreain,A., deoliveira,P.S., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunsreain,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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IL3-UT0117-160301-502-G10 UT0117 Homo sapiens cDNA, mRNA sequence.
B1062368
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                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.inh.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                         1 (bases I to 417)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="poorly differentiated adenocarcinoma with signet ring cell features" /lab_host="DH10B"
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Ludwig Institute for Cancer Research
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/db_xref="taxon:9606"
/clone="IMAGE:2256157"
/clone_lib="NCI_CGAP_Gas4"
                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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Unpublished (1997)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
11 (bases 1 to 484).
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40nl3 fwd. Fr from Amersham High quality sequence stop: 448.

Location/Qualifiers
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/clone="IMAGE:1699540"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
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/lab_host="DH10B"
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Contact: Wilson RK
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AW971724 530 bp mRNA linear EST 01-JUN-2000 EST383813 MAGE resequences, MAGL Homo sapiens cDNA, mRNA sequence.
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RPCI-11-230P5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-230P5,
                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from ABACPAC Resources (http://becpac.med.buffalo.edu/ordering) or from Research Genet cs (hffo@tesgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 501)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
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                                                 Gaps
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                                                                                        Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Other GSSs: RPCI-11-230PS.TJ
Other GSSs: RPCI-11-230PS.TJ
Ochect: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
711: 301 838 0208
Fax: 301 838 0208
  Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                 0; Indels
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ilarity 100.0%; Pred. No. 1.8e-10;
Conservative 0; Mismatches 0;
1.6%; Score 52; DB 9; Lv
100.0%; Pred. No. 1.9e-10;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Lymphocytes"
/note="Vector: pBACe3.6;
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/db_xref="taxon:9606"
/clone="RPCI-11-230P5"
/clone_lib="RPCI-11"
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AW971724.1 GI:8161570
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         Query Match 1.6%
Best Local Similarity 100.0
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                  DNA sequence.
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Matches 52; Conserv
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BASE COUNT
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                                                                                                                                                                                                                               Gaspard, R., Gay, C., Holt
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 545)
                                                                                                                                                                                                                                                                                                                                  Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                            1 (bases 1 to 530)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Ga, J. E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="MAGE resequences, MAGL"
/note="Vector: pBluescriptSKm"
139 c 111 g 145 t
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High Throughput Sequencing Center
University of Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: johnq@tigr.org
Plate: 294
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                                                                              Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                REFERENCE
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/note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites" 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eoc RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHW, pregnant uterus NbHPU, and fetal heart NbHH19W) were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization the driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools 340488-345479, and 484488-489479.
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Eukaryorta.

Eukaryorta.

Eukaryorta.

Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 583)

NCI-GAAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:1661017"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length. 470 Extor: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 411.
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1.6%; Score 52; DB 12; Length 545;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                             /clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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                                                                                                                                                                                 /clone="Plate=895 Col=20 Row=E"
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                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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                                                High quality sequence stop: 545.
Location/Qualifiers
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/lab_host="DH10B"
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Unpublished (1997)
Seg primer: T7
Class: BAC ends
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 171)

S Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)

Unpublished (1998)

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ198714 171 bp DNA linear GSS 20-APR-1999 RPCII1-59J23.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-59J23, DNA sequence.
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 753)
Xiao, H., Peng, Y., Song, H., Gu, Y., Yang, Y., Gao, G., Xu, X., Li, N., Gao, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Chen, Z. and Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
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                                                                                                                                                                      Homo sapiens cDNA FHTB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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1.6%; Score 52; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 52; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="FHTBABH02"
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/lab_host="BM25.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="FHTB"
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AQ198714.1 GI:3610913
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                                                                                                                                                                                                                                                                                                                               AQ589333 717 bp DNA linear GSS 07-JUN-1999 CITBI-E1-2645K6.TF CITBI-E1 Homo sapiens genomic clone 2645K6, DNA
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Venter, J.C.
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1. (bases 1 to 717)
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/note="vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
Calrech Human BAC Library D"
175 c 140 g 180 t
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                                                                  Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                     1.6%; Score 52; DB 9; Le
100.0%; Pred. No. 1.7e-10;
tive 0; Mismatches 0;
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/db_xref="taxon:9606"
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/clone_lib="CITBI-El"
/sex="male"
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Hillder,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ac52b01.s1 Stratagene fetal retina 937202 Homo sapiens CDNA clone
IMAGE:866185 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="Solk (kanamycin resistant)"
/note="Vector: pBluescript Sk-; Site_1: EcoRI; Site_2:
Xho!; Cloned undirectionally Primer: Oligo dr. Pooled
retinal tissue. Average insert size: 1.0 kb; Uni-ZaP xR
Vector; -5' adaptor sequence: 5' GAATTGGGCACGAG 3' -3'
adaptor sequence: 5' CTGAGTTTTTTTTTTTTTTTT 3'"
                                                                                                                                      /note="vector: pBaCe3.6; Site_1: ECORI; Site_2: ECORI; RPCIll Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@inage.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 216.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                              Score 51; DB 12; Length 171;
Pred. No. 8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:866185"
/clone_lib="Stratagene fetal retina 937202"
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100.0%; Pred. No. 6.9e-10
ative 0; Mismatches 0
                                                                                                                                                                                                                                  Query Match
1.6%; Score 51; Db
Best Local Similarity 100.0%; Pred. No. 8e-
/organism="Homo sapiens"
/db_xref="GDB.752510"
/db_xref="taxon:9606"
/clone="RPCI-11-59273"
/clone_lib="RPCI-11"
                                                                                                                    /cell_type="Lymphocytes"
/note="Vector: pBACe3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 bp
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AAĞ62976.1 GI:2616967
                                                                                                      /sex="Male"
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Contact: Wilson RK
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KEYWORDS
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H90008

108 A3403.51 Soares fetal liver splean INFLS Homo sapiens CDNA clone INPES 1040389 3' similar to contains Alu repetitive element; contains MERZO repetitive element; mRNA sequence.
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/lab_host="Original lampicillin resistant)"

/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)

/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)

/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)

/note="Organial property of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of the pact of 
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1 (bases 1 to 30)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston The WashUrWerck EST Project
Unpublished (1995)
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Insert Size: 1095
High quality sequence stops: 320
Source: IMAGE Consortium, Linl.
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1095 std Error: 0.00
Seq primer: Promega -21ml3
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="Soares fetal liver spleen lNFLS"
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/dev_stage="20 week-post conception fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 360;
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1.6%; Score 51; DB 10; I
Best Local Similarity 100.0%; Pred. No. 5.5e-10;
Matches 51; Conservative 0; Mismatches 0;
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/db_xref="GDB:3789342"
/db_xref="taxon:9606"
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Location/Qualifiers
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H90008.1 GI:1080438
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RESULT 43

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Gaps

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Indels

6.9e-10; thes 0;

51; Conservative

Matches

Best Local Similarity

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DNA sequence.
A0280600
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Best Local Similarity
Matches 51; Conserv
                              Simpson, A.J.
                                                                                                                                                                     20202663
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                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:841103"
/clone="IMAGE:841103"
/sex="mail="Stratagene lung (#937210)"
/sex="mail="Stratagene lung (#937210)"
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1 (bases 1 to 375)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Eriones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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                                                                                                                                                                                                                                                                                                                            Bukaryott, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 369)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Wahite,Y., Wylie,T., Waterston,R. and Wilson,R.
Unpublished (1997)
Contact: Wilson RK
                              EST 06-MAR-1998
                              AA486970 369 bp mRNA linear EST 06-MAR-199 ab17f12.rl Stratagene lung (#937210) Homo sapiens CDNA clone IMAGE:841103 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert.Length: 2381 Std Brror: 0.00
Seg primer: -26ml3 rev1 Er from Amersham
High quality sequence stop: 361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1190 cccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcc 1240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                               AA486970.1 GI:2217134
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BF924753/C
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ORIGIN
                                                                       DEFINITION
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AA486970/c
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JOURNAL
                                                                                                                                                                                                                      VERSION
KEYWORDS
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Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
Site_2: Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
a 94 c 113 g 69 t
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                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CML&t2-CMI-NT0209-281100-609-c10&t3=2000-11-28&t4=1)
Seq primer: puc 18 forward: 15
High quality sequence start: 15
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 379)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ280600 379 bp DNA linear GSS 22-NOV-1 CITBI-E1-2516H22.TR CITBI-E1 HOMO Sapiens genomic clone 2516H22,
                                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 375;
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Other_GSSs: CITBI-E1-2516H22.TF
Other_Hark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; L
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100.0%; Pred. No. 5.4
vative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ280600.1 GI:3906419
                                                                                                                                                                                                                                                                                                                                                  rel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Clones are available from Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search.html.

Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers

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Source
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Homo sapi

Sequence

Sequence Homo sapi Sequence

AX351033

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Sequence

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Sequence Homo sapi

Homo sapi Sequence

AX060719

Scoring table:

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Sequence Sequence Sequence Sequence

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Sequence

AX060713 : AX060892 : AF285167 E

Sequence

Homo sapi

Homo sapi Homo sapi

Sequence Sequence

AX127764 SAX139751 SAF258627 BAB055982 BAX253452 AX092594 SAX135712 SAX135712

Sequence

Sequence Sequence

Sequence

AX127830 AX139817

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I (sites)
Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P.,
Rosier-Montus, M.F., Remaley, A. and Santamarina-Fojo, S.
Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 2 08-NOV-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhlni; Hominidae; Homo.
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PAT 06-FEB-2002

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Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 5 08-NOV-2001;

Aventis Pharma S.A. (FR)

JOURNAL FEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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ACCESSION

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Cablo 1274, UN. E-meal. enquiries: numquery esanger.ac.uk clonerequestes: clonerequestes assembly data is compared from overlapping clones. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with mis sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBE; Sw. SWISSPROT; Tr., TREMBL; WP., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 mapping betto.
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   NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Sequencing vector: M13; M77815; 100% of reads
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Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; sum-of-contigs
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http://frp.genome.washington.edu/RW/RepeatWasker.html
  Contact: sequence_submissions@genome.wi.mit.edu
   All repeats were identified using RepeatMasker:
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Qiu,Y., Cavelier,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F. Human and mouse aboal comparative sequencing and transgenesis studies revealing novel regulatory sequences

Genomics 73 (1), 66-76 (2001)
   Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M. Compositions and methods for modulating hdl cholesterol and triglyceride levels Patent: WO 0115676-A 1 08-MAR-2001; University of British Columbia (CA); Xenon Genetics Inc. (CA) Location/Qualifiers
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Jirect Submission

All repeats were identified using Repeatmasker:
Smit, A.F.A. & Green, P. (1996-1997)
Smit, A.F.A. & Green, P. (1996-1997)
  Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
  arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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contig of 905 bp in length
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   Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P., Brewer, B., Duvergor, N., Remaley, A. and Santamarina-Fojo, S. Regulatory nucleic acid sequences of the abcl gene Patent: WO 0183746-A 7 08-NOV-2001;
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Pullinger,C.R., Hakamata,H., Duchateau,P.N., Eng,C.,
Aouizerat,B.E., Fielding,C.J. and Kane,J.P.
Analysis of haBc1 gene 5' end: additional peptide sequence, promoter region, and four polymorphisms
Puchem. Blophys. Res. Commun. 271 (2000) In press
2 (bases 1 to 200)
Pullinger,C.R., Hakamata,H., Duchateau,P.N., Eng,C.,
  Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S. Regulatory nucleic acid sequences of the abol gene patent: WO 0183746-A 8 08-NOV-2001;
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Submitted (23-JUN-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 94143-0130, USA
Sequence update by submitter
Location/Qualifiers
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Patent: WO 0078972-A 1 28-DEC-2000;
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Lawn, R. M., Wade, D., Oram, J. F. and Garvin, M. Atp binding casette transporter protein abcl polypeptides Patent: WO 0079971-A 1 28-DEC-2000; CV THERAPEUTICS, INC. (US)
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PAT 22-JAN-2001

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1 (bases 1 to 10474)
Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
Arb binding cassette transporter protein abcl polypeptides
Patent: WO 0078971-A 7.28-DEC-2000;
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Patent: WO 0078971-A 9 28-DEC-2000;
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Lawn, R.M., Wade, D. and Garvin, M.
Regulation with binding cassette transporter protein abcl Patent: Wo 0070872-A 9 28-DEC-2000; CV THERAPEUTICS, INC. (US)
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I (Dases I to 10474)
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Regulation with binding cassette transporter protein abcl Patent: WO 0078972-A 7 28-DEC-2000;
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Zhao,L.X., Zhou,C.J., Tanaka,A., Nakata,M., Hirabayashi,T.,
Amachi,T., Shioda,S., Ueda,K. and Inagaki,N.
Cloning, characterization and tissue distribution of the rat
ATP-binding cassette (ABC) transporter ABCZ/ABCA2
Blochem. J. 350 (Pt 3), 865-872 (2000)
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PAT 15-MAY-2001

linear

DNA

Sequence 3 from Patent W00130848. AXI27764

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AX127764

ACCESSION VERSION

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artificial sequence.

(bases 1 to 446)

Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H., Remaley, A., Brewer, H.B. and Dean, M. Nucleic acids of the human abcl gene and their therapeutic and diagnostic application

L. Patent: WO 0130848-A 3 03-MAY-2001;
Aventis Pharma S.A. (FR)

Location/Qualifiers
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Denefie,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
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Remaley,A., Brewer,H.B. and Dean,M.
Nucleics acids of the human abcl gene and their therapeutic and
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Patent: EP 1096012-A 3 02-MAY-2001;
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Submitted (20.FEB-2001) Kazumitsu Ueda, Kyoto University Graduate
School, Applied Life Sciences; Kitashirakawa, Kyoto Sakyo-ku, Kyoto
606-8502, Japan (E-mail:uedak@kais.kyoto-u.ac.jp,
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   Tanaka, A. R., Abe-Dojmae, S., Arakawa, R., Sadanami, K., Kidera, A., Kioka, N., Amachi, T., Yokoyama, S. and Ueda, K.
A new topological model of functional human ABCA1-Signal peptide
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   Pullinger, C.R., Hakemata, H., Duchateau, P.N., Eng, C., Anouserath, B.E., Fielding, C.J. and Rane, J.P.
Analysis of hABCl gene 5' end: additional peptide sequence, promoter region, and four polymorphisms
Biochem. Biophys. Res. Commun. 271 (2000) In press 2 (bases 1 to 697)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
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Attie-A.D., Cook.M., Gray-Keller,M.P., Hayden,M.R., Pimstone,S. and Brooks-Wilson,A.
Abcl modulation for the modulation of cholesterol transport Patent: WO 0131284-A 1 10-MAY-2001,
WISCONSIN ALUMNI RESERREL FOUNDATION (US)
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   PAT 30-MAY-2001
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Denefle, P. Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemonine, C., Duverger, N., Jaye, M., Searfoss, G.H., Remaley, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and
  1 (bases 1 to 9741)
Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., searfoss 111, G.H.,
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1 (bases 1 to 7260)
Schmitz,G. and Bodzioch,M.
Atp binding cassette transporter 1 (abcl) gene polymorphisms and uses thereof for the diagnosis and treatment of lipid, cardiovascular or inflammatory disorders
Patent: WO 0170810-A 3 27-SEP-2001;
Bayer Aktiengesellschaft (DE)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 7860)

Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M. Compositions and methods for modulating hdl cholesterol and Pringlyceride levels

Patent: WO 0115676-A 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)
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Patent: WO 0130848-A 70 03-MAY-2001;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9654)
Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
   Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S. Regulatory nucleic acid sequences of the abcl gene Patent: Wo 0183746-A 10 08-NOV-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
  Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    Remaley,A., Brewer,H.B. and Dean,M.

Nucleics acids of the human abcl gene and their therapeutic and diagnostic application
Patent: EP 1096612-A 69 02-MAY-2001;
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  Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Naqai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
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1 (bases 1 to 9854)
Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C., Naudin,L., Lemoine,C., Duverger,N., Jaye,M., searfoss Iii,G.H., Remaley,A., Brewer,H.B. and Dean,M.
diagnostic application
Patent: Ep 109612-A 70 02-MAY-2001;
Aventis Pharma S.A. (FR)
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   1 others
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LLSICASVPKVEFHERHILEHFSFCVCVSVSLFPAKGIVSFSWASFRIWVLWKAVFWQ
HGESMAYWEGQLGLGLNIAFEFFILDVG"
   ö
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Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A. NEDO human cDNa sequencing project Unpublished (2000)
2 (bases 1 to 1556)
   1 (bases 1 to 37)
Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
Gompositions and methods for modulating hdl cholesterol and
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Patent: WO 0115676-A 255 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)
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Synthetic construct
artificial sequence.
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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artificial sequence.
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Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
Compositions and methods for modulating hdl cholesterol and trigityceride levels
Patent: WO 0115676-A 253 08-WAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)
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   ö
   ö
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Stojanovic, N., Straues, M., Stange-Thoman, N., Travers, M., Travers
   ..... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
  NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Insert size: 206759; sum-of-contigs
Quality coverage: 9.6 in Q20 bases; agarose-fp
Quality coverage: 9.5 in Q20 bases; sum-of-contigs
   Sequencing vector: Plaamid; n/4; 100% of reads Sequencing vector: Plaamid; n/4; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 20576 bases at least Q40 Consensus quality: 20578 bases at least Q20 Consensus quality: 20618 bases at least Q20
  Contact: sequence submissions@genome.wi.mit.edu Project Information Center project name: L13324
  1431 1530; gap of 100 bp
1531 4604; contig of 2474 bp in length
4005 4104; gap of 100 bp
4105 4132075; contig of 127971 bp in length
  132076 132175: gap of 100 bp 132176 135638: contig of 3463 bp in length 135639 135739 ap of 100 bp 141622 141721: gap of 100 bp 141622 147721: gap of 100 bp 141722 157897: contig of 16086 bp in length 141722 157807: contig of 16086 bp in length 141722 157807: contig of 16086 bp in length
   157808 157907: gap of 100 bp
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Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abcal)
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   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 278572)
Qiu, Y., Cavelier, L., Chiu, S., Yang, X., Rubin, E. and Cheng, J.F. Human and mouse abcal comparative sequencing and transgenesis
  2 (bases 1 to 278572)
Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submitted (14-JUL-2000) Genome Science Department, Lawrence
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Homo sapiens BAC clone GS1-234B20 from 7q31.1-q31.3, complete
  PAT 26-SEP-2001
  ö
   Direct Submission
Submitted (09-JAN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
   Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
Low density liprotein binding proteins and their use in diagnosing and treating atherosclerosis
Patent: Wo Ol64874-A 50 07-SEP-2001;
Boston Heart Foundation, Inc. (US)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 12425)
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 1842?) Sulston,J.E. and Waterston,R.
   Gaps
  Gaps
                                      ö
   ö
7.6%; Score 27; DB 10; Length 278572; 100.0%; Pred. No. 0.00044; tive 0; Mismatches 0; Indels 0;
  6.7%; Score 24; DB 6; Length 12425; 100.0%; Pred. No. 0.022; Live 0; Mismatches 0; Indels (
  linear
  Maupin,R., Bauer,C. and Le,T.
The sequence of Homo sapiens BAC clone GSI-234B20
  DNA
   Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
   Sequence 50 from Patent WO0164874.
   2594
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/db_xref="taxon.9606"
3702 c 3566 g 2594
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  88 tttatctttcagttaatgaccagccac 114
  2395 GGAGGAGGGAGGGAGGAAGGAAG 2418
  326 ggaggaggaggaggaaggaag 349
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  AC006326
AC006326.2 GI:4508133
  (bases 1 to 18427)
   3 (bases 1 to 18427)
Waterston, R.H.
  MO 63108, USA
4 (bases 1 to 18427)
   Ouery Match
Best Local Similarity 100.(
Matches 24; Conservative
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  1. .12425
   Homo sapiens
                  1 Similarity
27; Conserv
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  Unpublished
   2563 a
  sednence.
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   human.
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JOURNAL
  REFERENCE
  AUTHORS
   MEDLINE
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  AUTHORS
  JOURNAL
   AUTHORS
  REFERENCE
  REFERENCE
  FEATURES
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  ORIGIN
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TITLE

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repeat_region
  selection: chloramphenicol NEIGHDRIA SEQUENCE INFORMATION: NEIGHDRIA SEQUENCE INFORMATION: The clone sequenced to the left is RP5-866N18, 200 bp overlap; clone sequenced to the right is CTA-343P13, 200 bp overlap. The actual start is unknown, the first known base of overlap is at base position 139224 of RG114A06; actual end is at 53881 of CTA-343P13. Location/Qualifiers
   The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@hhgri.nih.gov , or see http://genome.wustl.edu/gsc
   Submitted (10-JUL-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA (bases 1 to 18427)
  Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington
Missouri 41.4 Errors Park Avenue. St. Louis, Missouri 63108, USA
  JUNIALITIES (UI-MAY-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA (c. bases 1 to 18427)
  Submitted (24-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
   NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
   all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
  This clone is from the first BAC library from Genome Systems, Inc. (http://www.genomesystems.com).
Cell line: lymphoblastoid
Haplotypes: two
   This sequence was finished as follows unless otherwise noted:
  University, 4444 Forest Park Avenue, St. Louis, Missouri 6
On Mar 24, 1999 this sequence version replaced 91:4138782.
  Center: Washington University Genome Sequencing Center
   Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
   Center project name: H_GS234B20
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/clone="GS1-234B20"
   ----- Genome Center
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  Center code: WUGSC
   (bases 1 to 18427)
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  SOURCE INFORMATION:
  restriction digest.
   1. .18427
  pBeloBAC
  Direct Submission
   Direct Submission
   Direct Submission
   Waterston, R.
   Waterston, R.
  Waterston, R.
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FEATURES

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  .10860
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repeat_region
  FEATURES
   ALECT COMMITTED AND ADDRESS OF THE ADDRESS OF THE ADDRESS OF ADDRESS OF THE ADDRE
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   complement(16664...)=16891)
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   http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90582)
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  Gaps
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  Human DNA sequence from clone RP5-1098C18 on chromosome 1p36.23-36.33, complete sequence.
  Length 18427;
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3991 c 3520 g 5795 t
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  /evidence=not_experimental
/protein_id="AAD28351.1"
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  3652 GGAGGAGGGAGGGAAGGAAG 3629
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Matches 24; Conservative
   Thomas, D.
Direct Submission
  Homo sapiens
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  gene
  ACCESSION
   REFERENCE
   AUTHORS
  JOURNAL
   AL583882
  KEYWORDS
  VERSION
  COMMENT
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Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1 http://www.sanger.ac.uk/HGP/Chr1 FP5-1098C18 is.from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pCYPAC2
   This sequence is the entire insert of clone RP5-1098C18 The true right end of clone RP11-154H17 is at 1402 in this sequence. Location/Qualifiers
  8740. .8801
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8864. .9575
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9646. .10004
   3462. .3740
/nocte="LiPB2 repeat: matches 5861. .6155 of consensus"
3890. .3991
/note="MER20 repeat: matches 118. .218 of consensus"
  314. .6690 "note="LIMC3 repeat: matches 5437. .5825 of consensus"
   7301. 7532
/note="AluJo repeat: matches 63. 291 of consensus"
7540. 8738
/note="LiMc3 repeat: matches 5843. .7037 of consensus"
  note="L1M4 repeat: matches 3850. .3937 of consensus"
   4909. .4961
/note="L2 repeat: matches 1. .52 of consensus" 5551. .5610
5552. .5607
/note="6 copies 10 mer tacacacaca 76% conserved" 700te="14 copies 4 more-
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10015. .10187
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10338. .10458
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11856. .11944
   6702. .6989
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6922. .7237
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  183. 1286
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   .90582
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/note="AluSq repeat: matches 1. .312 of consensus"
/note="AluSq repeat: matches 1. .312 of consensus"
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/note="43 copies 4 mer ggaa 70% conserved" note="L1PA11 repeat: matches 5310. .6159 of consensus" 14026. .14125 /note==10 copies 10 mer gagagaaaga 72% conserved" /note==11M4 repeat: matches 4694. .5255 of consensus" 14024. .14956 /note=="Illabar repeat: matches 6153. .6183 of consensus" /14957. .15266 /note="LIMB3 repeat: matches 5792. .6153 of consensus" 15853. .16166 /note="MER91A repeat: matches 18. .196 of consensus" 30627. .30905 /note="L2\_repeat: matches 2466. .2497 of consensus" 33150. .33215 /note="MER74A repeat: matches 1. .558 of consensus" 29282. .29456 /note="Alusg repeat: matches 18. .296 of consensus" 32695. .32726 // 1/22. .1/3b4 // 1/22. .1/3b4 // 1/22. .19068 // 1/22. .19068 /note="MLT1D repeat: matches 17. .505 of consensus" 28426. .28538 Anote="Alusp repeat: matches 1. .311 of consensus" 15267. .15610 "AluSx repeat: matches 1. .311 of consensus"
6201. .16511
fnote="AluY repeat: matches 1. .311 of consensus"
17222 .17364 19975. .19990 7note="MITIC repeat: matches 1. .466 of consensus" 2008. .20189 7note="23 copies 4 mer gatg 64% conserved" 22885. .23136 /note="MIR repeat: matches 52. .114 of consensus" 34512. .34640 note="MLTLJ repeat: matches 8. .330 of consensus" 9575. .19996 note="MIR repeat: matches 81. .212 of consensus" 27909. .28364 note="MIR repeat: matches 28. .149 of consensus" 8764. .29250 22964. .23123
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23620. .23682. .23682
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7note="Cpg island"
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AF179296 123339 bp DNA linear HTG 08-OCT-1999
Homo sapiens, *** SEQUENCING IN PROGRESS ***, in ordered pleces.
AF179296
  ö
   Direct Submission Submission Submitted (20-MG-1999) Genome Analysis, Institute of Molecular Submitted (20-MG-1999) Genome Analysis, Institute of Molecular Bottechnology, Beutenbergstrasse 11, Jena 07745, Germany contig 1: pos. 1 - 92151 contig 2: pos. 92152 - 123339 Inbetween a gap of unknown size.
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
  //octe="Alusq/x repeat: matches 1. .139 of consensus" 35129. .35212 //octe="MINSQ/x repeat: matches 1. .84 of consensus" 35287. .35769 repeat: matches 5812. .6290 of consensus" 35772. .35847 //octe="Alusay repeat: matches 226. .299 of consensus" 35853. .35924
  ( Dases I to 123339)
Schudy, A., Platzer, M., Solilhabel, M., Koczan, D., Thiesen, H.-J.,
Merck-Rousseau, M.F., Baumgart, C., Menzel, U., Weber, J.,
Schattevoy, R. and Rosenthal, A.
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  /note="FAM repeat: matches 116. .173 of consensus" 34766. .34906
   /note="MLT2B repeat: matches 1. .73 of consensus"
   * NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
  ö
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:045. .1119
   566. .636 /
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   TITLE
   LOCUS
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| repeat_region repeat_region repeat_region repeat_region repeat_region | ែ។ ។ ។ ។ ។ ។                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | perlined to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr |

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LOCUS

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Direct Submission

AL Submitted (10-7aN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Esbarich 320 Charles Street, Cambridge, MA 02141, USA

Essarch, 320 Charles Street, Cambridge, MA 02141, USA

Essarch, S. Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barra,N. Bastlen,V. Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Brown,A., Canarata,D., Collogel, C., Dodge,P., DeArellano,K., Dear,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,M., Gage,D., Galagan,J., Gardyna,S., Gorde,B., Hoaford,A., Horton,L., Hulme,W., Illev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Macdonald,P., Major,J., Marquis,N., Matthews,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., Norbu,C., Setta,R., Reback,M., Rieback,M., Pollara,V., Senera,N., Shera,R., Schauer,S., Schupback,R., Stange-Thomann,N., Stojanovic,N., Stannon,J., Zenber,M., Travis,N., Tr
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  Submitted (18-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jan 10, 2002 this sequence version replaced gi:15983570.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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repeat\_region

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  FEATURES
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```
Direct Submission

Direct Submission

Librated (09-0CT-2000) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

On Aug 21, 2000 this sequence version replaced gi:9856693.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
annotated human repeats but not necessarily within known
sequence is ambiguous, there is an annotation using the 'unsure'
   ó
  Human DNA sequence from clone RP11-5N23 on chromosome 10p14-15.3 Contains ESTs, GSSs, STSs and a CpG island. Contains the 5' part of the PRKCQ gene for protein kinase C theta and a novel gene,
  PRI 12-OCT-2000
  The following abbreviations are used to associate primary accession
  IMPORTANT: This sequence is not the entire insert of clone RP11-5N23 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP11-5N23 is at 132741 in this sequence. The true left end of clone RP11-55478 is at 102011 in this sequence. The true right end of clone RP11-55478 is at 100 in
  http://www.sanger.ac.urk/HGP/Chri0
RP11-5N23 is from the library RPCI-11.1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 132741)
   numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
   Gaps
  ö
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  REFERENCE
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misc\_feature

CDS

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32062. 32097

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complement(22776. .23021)
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Gaps

RESULT

SOURCE

COMMENT

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BASE COUNT
   RESULT 45
  DEFINITION
  SOURCE
ORGANISM
   source
   ACCESSION
   TITLE
JOURNAL
   REFERENCE
  AUTHORS
  AL353893
   KEYWORDS
  VERSION
   FEATURES
   COMMENT
                           ORIGIN
   δλ
   AL Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 18A, UK. E-mail enquiries.

Cambridgeshire, CBIO 18A, UK. E-mail enquiries.

Cambridgeshire, CBIO 18A, UK. E-mail enquiries.

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >-

as compressions and repeats; all regions were covered by at least

as compressions and repeats; all regions were covered by at least

as compressions are used to associate primary accession numbers given

in the feature table with their source databases: Em: EMBL; Sw:

SWISSPROT: Tr:, TREMBL; WP:, WORNBEP; Information on the WORNPEP;

http://www.conf.ac.
  /note="Tandem repeat. Forced join. Gap size estimated to be approximately 90bp by restriction digest data." complement(134059. .134062)
/note="Single clone region. Assembly confirmed by restriction digest data." complement(134064. .134068)
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/note="Single clone region. Assembly confirmed by restriction digest data."
  AL163512 134334 bp DNA linear ROD 17-NOV-2001
Mouse DNA sequence from clone RP21-466E12 on chromosome X, complete
  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP21-468E12 is from the RPCI-21 Mouse PAC Library constructed by the group of Pieter de Jong.
  /note="Tandem repeat. Forced join, Gap size estimated to
be approximately 280bp by restriction digest data."
114512
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        19957

  /clone_lib="RPCI-21"
15023
  Location/Qualifiers
1. .134334
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   (bases 1 to 134334)
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  house mouse.
   sednence.
   Wall M.
   misc_feature
  misc_feature
   misc_feature
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   misc_feature
  DEFINITION
   Source
  ORGANISM
  ACCESSION
   VERSION
KEYWORDS
  REFERENCE
   AUTHORS
  AL163512
  JOURNAL
   FEATURES
```

```
AL353893 137072 bp DNA linear HTG 10-JUL-2001
HOMO sapiens chromosome 1 clone RP5-1108E5, *** SEQUENCING IN
PROGRESS ***, 6 unordered pieces.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jul 15, 2000 this sequence version replaced gi:8052073.
  0; Gaps
   Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 134274 bases at least Q40
Consensus quality: 135563 bases at least Q20
Consensus quality: 135563 bases at least Q20
Insert size: 136572; sum·of-contigs
Insert size: 136572; sum·of-contigs
Quality coverage: 4.52x in Q20 bases; sum-of-contigs Quality
coverage: 4.50x in Q20 bases; agarose-fp
  * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
   6.7%; Score 24; DB 10; Length 134334;
100.0%; Pred. No. 0.024;
tive 0; Mismatches 0; Indels 0;
   68025 71010: contig of 2986 bp in length 71011 7110: gap of 100 bp 71011 89837: contig of 2986 bp in length 71011 89837: contig of 100 bp 100 bp 113011 113010: contig of 23073 bp in length 113011 113010: contig of 23073 bp in length 113111 1137072: contig of 23962 bp in length.
  4286 4385: gap of 100 bp
4386 67924: contig of 63539 bp in length
  4285: contig of 4285 bp in length
41709 a 26034 c 25611 g 40980 t
   Contact: humquery@sanger.ac.uk
  Center code: SC
Web site: http://www.sanger.ac.uk
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Matches 24; Conservative
   be preserved.
  Homo sapiens
   AL353893
   Mclay, K.
   human.
  Query Match
```

Search completed: September 20, 2002, 06:30:00 Job time: 18394 sec

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us-09-846-456-2.oli.rng

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September 20, 2002, 06:06:55; Search time 521.76 Seconds
(without alignments)
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|    | Description                 | Human ABC1 gene ex | Human ABC1 genomic | Nucleotide sequenc | Nucleotide sequenc | Nucleotide sequenc | Nucleotide sequenc | Nucleotide sequenc | Nucleotide sequenc | Partial human ABC1 |
|----|-----------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|    | ΩI                          | AAC69132           | AAF92831           | AAF24680           | AAF24702           | AAF24685           | AAF24686           | AAF24707           | AAF24708           | AAS04035           |
|    | DB                          | 21                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 |                    | 22                 |
|    | Query<br>Match Length DB ID | 44.5 10545         | 183999             | 10442              | 10442              | 10474              | 10474              | 10474              | 10474              | 446                |
| фP | Query<br>Match              | 44.5               | 44.5               | 21.6               | 21,6               | 21.6               | 21.6               | 21.6               | 21.6               | 16.8               |
|    | Score                       | 159                | 159                | 77                 | 77                 | 77                 | 77                 | 77                 | 77                 | 09                 |
|    | Result<br>No.               | 7                  | 7                  | m                  | 4                  | S                  | 9                  | 7                  | - σο               | σ                  |

| Human ABCA1 homolo<br>Human polynucleot1 |          |          | polyn    |          |          | ABC1     | -        | ABC1     | ABC1     | ABC1     | ABC1     | ABCI     | ABC1     |          | c        |          |          | Human low density | Human BMP-4 5, ups | DNA sequence from | M        | BMP4, Rattus ratt | Bone morphogenetic | Sequence encoding | Prepro human CBMP2 | Human CBMP2(b) CDN | Human osteogenic p | Human prepro CBMP2 | Human osteogenic p | DNA encoding novel | Human bone morphog | one Mor  | BMP-2B   | Human BMP-2B seque |
|------------------------------------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-------------------|--------------------|-------------------|----------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|
| ABA09200<br>AAK52667                     | AAD21326 | AAI70315 | AAK51683 | AAC69388 | AAF83826 | AAF92835 | AAC69387 | AAC69120 | AAC69385 | AAC69386 | AAC69389 | AAS06120 | AAS06121 | AAH07432 | AAH18606 | AAF93084 | AAF93082 | AAH26495          | AAZ39175           | AAC83229          | AAV32783 | AAQ32853          | AAV01680           | AAQ53144          | AAQ72710           | AAT02601           | AAV15207           | AA227580           | AAX00232           | AAS79379           | AAT78942           | AAN80634 | AAQ14037 | AAQ31870           |
| 22                                       | 22       | 22       | 22       | 21       | 22       | 22       | 21       | 21       | 21       | 21       | 21       | 22       | 22       | 22       | 22       | 22       | 22       | 22                | 21                 | 22                | 13       | 13                | 19                 | 14                | 15                 | 17                 | 19                 | 20                 | 20                 | 23                 | 18                 | 0        | 12       | 13                 |
| 7086                                     | 7260     | 7260     | 7281     | 7857     | 7860     | 7860     | 7861     | 7864     | 7864     | 7864     | 7864     | 9741     | 9854     | 736      | 1556     | 37       | 38       | 12425             | 30                 | 1077              | 1456     | 1751              | 1751               | 1788              | 1788               | 1788               | 1788               | 1788               | 1788               | 1832               | 1944               | 1954     | 1954     | 1954               |
| 16.8                                     |          |          |          |          |          |          |          |          |          |          |          | 16.8     | 9        | 4        | 4        |          | 8.6      |                   |                    |                   |          | 6.2               |                    |                   |                    |                    |                    | 6.2                |                    |                    | •                  |          |          | •                  |
| 09                                       | 09       | 09       | 9        | 09       | 9        | 09       | 9        | 09       | 9        | 09       | 09       | 9        | 9        | 51       | 51       | 35       | 35       | 24                | 22                 | 22                | 22       | 22                | 22                 | 22                | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22       | 22       | 22                 |
| 10                                       | 12       | 13       | 14       | 15       | 16       | 17       | - 1 - 2  | 19       | 20       | 21       | 22       | 23       | 24       | 25       | 26       | 27       | 28       | 29                | 30                 | c 31              | 6        | 33                | 34                 | 35                | 36                 | 37                 | 38                 | 39                 | 40                 | c 41               | 4                  | 43       | 44       | 45                 |

## ALIGNMENTS

```
Human ABC1 cholesterol transporter; chromosome 9q31; promoter; ATP-binding cassette; HDL deficiency disorder; high density lipoprotein; Tangler disease; TD; familial HDL deficiency; FHA; polymorphism; cardiovascular disease; coronary artery disease; coronary restenosis; cerebrovascular disease; peripheral vascular disease; Alsmann-Pick disease; Huntington's disease; X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prophylaxis; drug screening; transgenic animal; ss.
  Human ABC1 gene exon 1 (promoter).
                        AAC69132 standard; DNA; 10545 BP.
  99US-0124702.
99US-0138048.
99US-0139600.
   15-MAR-2000; 2000WO-IB00532.
  99US-0151977
   29-JAN-2001 (first entry)
   WO200055318-A2
   15-MAR-1999;
08-JUN-1999;
17-JUN-1999;
01-SEP-1999;
  Homo sapiens.
  21-SEP-2000.
  AAC69132;
RESULT
AAC69132
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(first entry)

17-MAY-2001

Human ABC1 genomic DNA.

```
The invention relates to the human ABCI cholesterol transporter protein CC (888082) and to nucleic acid sequences (C69120) which encode it. ABCI is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly citracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol lefflux from the cell. The gene encoding ABCI is coracted on chromosome 9431, and mutations in this gene are associated involved in cholesterol efflux from the cell. The gene encoding ABCI is with two genetic HDL (high density lipoprotein) deficiency discases. CT angler disease (TD) and familial HDL deficiency (FHA). These diseases of an autosomal dominant trait. LOW levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly corromary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease. Coronary restenosis, and peripheral vascular disease. Coronary restenosis, and peripheral vascular disease. Cardiovascular disease. The invention provides genetic constructs and transgenic cells and mon-human animals comprising human ABCI nucleic cardiovascular disease comprising the administration of an expression coronary are an activity, compounds which minic ABCI expression and methods of sorteening for such compounds coronary cerebrovascular disease, coronary restenosis or peripheral vascular disease, Huntingcon's disease, "Viliked adrenoleukodystrophy and cerebrovascular disease, Huntingenome as GenBank Acce
  New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
   Hayden MR, Wilson AR, Pimstone SN;
   Claim 50; Fig 12; 229pp; English.
(UYBR-) UNIV BRITISH COLUMBIA. (XENO-) XENON BIORESEARCH INC.
  disease and cancer -
   WPI; 2000-587528/55
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ő 8240 tgittggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 8299 199 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 258 Gaps ö 44.5%; Score 159; DB 21; Length 10545; 100.0%; Pred. No. 2.3e-68; Live 0; Mismatches 0; Indels 0; 8360 ggggattggaggaggaggagggaaggaagctgtgttg 8398 319 ggggattggaggagggagggaaggaagctgtgttg 357 Conservative Best Local Similarity Matches 159; Conserv Query Match g ò à q ò

AAF92831 ID AAF92831 standard; DNA; 183999 BP

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RESULT

AAF92831;

Sequence 10545 BP; 2647 A; 2225 C; 2411 G; 3256 T; 6 other;

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diagnosed as having a lower than normal high density.

Lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity.

The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
  Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity .
  53328 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagaagaca 53387
  High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABCl; ds.
   199 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 258
  0; Gaps
   Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
  The present invention relates to a method for treating a patient
  44.5%; Score 159; DB 22; Length 183999; 100.0%; Pred. No. 2.3e-68; tive 0; Mismatches 0; Indels 0;
   Clee SM;
   53448 ggggattggaggaggagggagggaaggaagctgtgttg 53486
  319 ggggattggaggagggagggagggaaggaagctgtgttg 357
   Nucleotide sequence of a human ABC1 polypeptide.
   Hayden MR, Brooks-Wilson AR, Pimstone SN,
  AAF24680 standard; DNA; 10442 BP.
   Claim 8; Fig 1; 317pp; English.
   (UYBR-) UNIV BRITISH COLUMBIA
  15-MAR-2000; 2000US-0526193.
23-JUN-2000; 2000US-0213958.
  01-SEP-2000; 2000WO-IB01492.
  99US-0151977
   (XENO-) XENON GENETICS INC.
  (first entry)
  Matches 159; Conservative
  WPI; 2001-244356/25.
  Query Match
Best Local Similarity
   WO200115676-A2.
   Homo sapiens
  01-SEP-1999;
   08-MAR-2001.
  20-APR-2001
  AAF24680;
   AAF24680
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   QQ
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AAF24702 standard; DNA; 10442 BP.

AAF24702

(first entry)

20-APR-2001

AAF24702;

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The present sequence encodes a human adenosine triphosphate (ATP)

binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell

comembranes and utilises ATP hydrolysis to transport a wide variety of
substrates across the plasma membrane. ABC1 is a pivotal protein in

the apolipoprotein-mediated mobilisation of intracellular cholesterol

stores. ABC1 is defective in Tangler disease, a genetic disorder

characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is

cocalised to chromosome 9422-9431. The ABC1 genes and proteins are

useful for developing pharmaceutical agents for the treatment of heart

ciseal of other disorders associated with hypercholesterolemia and

therosclerosis. The genes are useful for developing screening assays

creen for compounds that regulate the expression of genes associated

with cholesterol transport. The genes and proteins are also useful for

are also useful as diagnostic indicators of cardiovascular disease and

cother disorders associated with hypercholesterolemia.
  Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
Human, adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9q22-9q31; heart disease; hypercholesterolemia;
   Length 10442;
   Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;
   21.6%; Score 77; DB 22; Length 10.
99.2%; Pred. No. 4.8e-28;
tive 0; Mismatches 1; Indels
  /product= "ABC1 polypeptide"
   atherosclerosis; cholesterol transport; ss.
  Disclosure; Page 122-128; 215pp; English.
   Location/Qualifiers
291..7076
  99US-0166573.
  Lawn RM, Wade D, Garvin M;
  99US-0140264.
   (CVTH-) CV THERAPEUTICS INC.
  99US-0153872
   16-JUN-2000; 2000WO-US16765
   Matches 127; Conservative
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   Best Local Similarity
   WPI; 2001-137812/14.
   atherosclerosis
   WO200078972-A2.
   18-JUN-1999;
  19-NOV-1999;
  Homo sapiens
  28-DEC-2000
  Query Match
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;
             0; Gaps
                         251 gacaaaca 258
                           349
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RESULT

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atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and
   Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
   substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangler disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 942-9431. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
  131 agctctggccgctgccttccagggctcccgagccacacyctgggcgtgctggctgaggga 190
  0; Gaps
   The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of
  Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangler disease; chromosome 9q22-9q31; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
  / Match 21.6%; Score 77; DB 22; Length 10442; Local Similarity 99.2%; Pred. No. 4.8e-28;
  Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;
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Pred. ----has 1; Indels
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   /product= "ABC1 polypeptide"
   0; Mismatches
  Claim 3; Page 117-123; 211pp; English.
  Garvin M;
   Location/Qualifiers
  99US-0140264.
99US-0153872.
99US-0166573.
  Cawn RM, Wade D, Oram JF,
   16-JUN-2000; 2000WO-US16591.
  (CVTH-) CV THERAPEUTICS INC.
   Matches 127; Conservative
  291..7076
  ø
  (UNIW ) UNIV WASHINGTON.
  /*tag=
   WPI; 2001-137811/14.
  P-PSDB; AAB31365
  atherosclerosis
  WO200078971-A2
  18-JUN-1999;
14-SEP-1999;
19-NOV-1999;
  Homo sapiens.
   28-DEC-2000
   Query Match
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Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
  Human; adenosine triphosphate binding cassette protein 1; ABC1;
apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
chromosome 9q22-9q31; heart disease; hypercholesterolemia;
atherosclerosis; cholesterol transport; ss.
  /product= "defective ABC1 polypeptide"
   Disclosure; Page 148-154; 215pp; English.
   Location/Qualifiers
323..7108
/*tag= a
  AAF24685 standard; DNA; 10474 BP.
  99US-0153872.
99US-0166573.
  Lawn RM, Wade D, Garvin M;
   16-JUN-2000; 2000WO-US16765
   99US-0140264
  (CVTH-) CV THERAPEUTICS INC.
   (first entry)
   WPI; 2001-137812/14.
                                       gacaaaca 258
   349 gacaaaca 356
   atheroscleros1s
  WO200078972-A2
  20-APR-2001
   Homo sapiens
  18-JUN-1999;
   14-SEP-1999;
19-NOV-1999;
   AAF24685;
                                     251
   AAF24685
   RESULT
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The present sequence encodes a human adenosine triphosphate (ATP)

binding cassette protein (ABC) 1 polypeptide, and is isolated from

a Tangier disease patient. ABC1 resides in cell membranes and utilises

ATP hydrolysis to transport a wide variety of substrates across the

combilisation of intracellular cholesterol stores. ABC1 is defective in

Tangier disease, a genetic disorder characterised by abnormal

HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome

of 942-9431. The ABC1 genes and proteins are useful for developing

pharmaceutical agents for the treatment of heart disease and other

disorders associated with hyperrolesterolesterolemia and atherosclerosis. The

chart regulate the expression of genes associated with cholesterol

transport. The genes and proteins are also useful for are also useful

as diagnostic indicators of cardiovascular disease and other disorders

as sociated with hypercholesterolemia.

Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

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ö
  The prosent sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide, and is isolated from a Tangter disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9422-9431. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other
   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and

    191 acatggcatgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaa
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   261 agetetggeegetgeetteeagggeteeegageeacacacgetgggegtgetggetgaggga 320
  Gaps
  Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
  Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
  ô
              Length 10474;
    /*tag= a
/product= "defective ABC1 polypeptide"
   Disclosure; Page 170-176; 215pp; English.
   Location/Qualifiers 323..7108
  AAF24686 standard; DNA; 10474 BP.
  99US-0140264.
99US-0153872.
99US-0166573.
  16-JUN-2000; 2000WO-US16765.
   Lawn RM, Wade D, Garvin M;
   (CVTH-) CV THERAPEUTICS INC.
  (first entry)
Query Match
Best Local Similarity 99.29
Matches 127; Conservative
  WPI; 2001-137812/14.
  381 gacaaaca 388
   251 gacaaaca 258
  atherosclerosis
   WO200078972-A2
   Homo sapiens.
  18-JUN-1999;
14-SEP-1999;
19-NOV-1999;
   20-APR-2001
   28-DEC-2000.
   AAF24686;
  9
  AAF24686
  Key
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disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
  Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
   agetetggeegetgeetteeagggeteeegageeaaegetgggegtgetgaggga 190
  261 agetetggeegetgeetteeagggeteeegageeacaegetgggegtgetggetgaggga 320
   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
  Gaps
   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
   Human; adenosine triphosphate binding cassette protein 1; ABC1;
  ;
0
  21.6%; Score 77; DB 22; Length 10474; 99.2%; Pred. No. 4.8e-28;
  Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;
  1; Indels
  /product= "defective ABC1 polypeptide"
  0; Mismatches
   Claim 27; Page 144-150; 211pp; English.
  Garvin M;
   Location/Qualifiers
  AAF24707 standard; DNA; 10474 BP
   99US-0153872.
   99US-0140264.
  Wade D, Oram JF,
   16-JUN-2000; 2000WO-US16591.
  99US-0166573
  CVTH- ) CV THERAPEUTICS INC
  (first entry)
  323..7108
  127; Conservative
   UNIW ) UNIV WASHINGTON.
   /*tag=
   WPI; 2001-137811/14.
P-PSDB; AAB31366.
  Similarity
  atherosclerosis -
  251 gacaaaca 258
   381 gacaaaca 388
   WO200078971-A2
   18-JUN-1999;
  Homo sapiens
  14-SEP-1999;
  19-NOV-1999;
  20-APR-2001
   28-DEC-2000
  Lawn RM,
  AAF24707;
   Query Match
   Local
   Matches
   131
  Key
  AAF24707
   RESULT
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                 Arguer transport a wide variety of substrates and utilises a rangler disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotral protein in the apolipoprotein mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in rangiler disease, a genetic disorder characterised by abnormal application of intracellular cholesterol stores. ABC1 is defective in rangiler disease, a genetic disorder characterised by abnormal phot-cholesterol metabolism. The ABC1 gene is localised to chromosome 9422-9431. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol as diagnostic indicators of cardiovascular disease and other disorders
  Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
  Gaps
  Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
      present sequence encodes a human adenosine triphosphate (ATP)
   ö
   Length 10474;
  Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;
  Indels
   "defective ABC1 polypeptide"
   21.6%; Score 77; DB 22; 99.2%; Pred. No. 4.8e-28;
  0; Mismatches
  associated with hypercholesterolemia.
  Location/Qualifiers
  AAF24708 standard; DNA; 10474 BP.
   (CVTH-) CV THERAPEUTICS INC. (UNIW ) UNIV WASHINGTON.
   16-JUN-2000; 2000WO-US16591.
  99US-0140264.
  99US-0153872.
   /*tag= a
/product= '
  (first entry)
  323..7108
  Matches 127; Conservative
  Query Match
Best Local Similarity
  251 qacaaaca 258
  381 gacaaaca 388
  WO200078971-A2
  Homo sapiens.
   18-JUN-1999;
  14-SEP-1999;
   19-NOV-1999;
  20-APR-2001
   28-DEC-2000
   AAF24708;
  Key
  AAF24708
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The present sequence encodes a human adenosine triphosphate (ATP)

binding cassette protein (ABC) 1 polypeptide, and is isolated from

a Tangier disease patient. ABC1 resides in cell membranes and utilises

ATP hydrolysis to transport a wide variety of substrates across the

care in the contract of the contract of substrates across the

mobilisation of intracellular cholesterol stores. ABC1 is defective in

Tangier disease, a genetic disorder characterised by abnormal

HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome

Sq22-9431. The ABC1 genes and proteins are useful for developing

planmaceutical agents for the treatment of heart disease and other

calsorders associated with hypercholesterolemia and atheroscierosis. The

genes are useful for developing screening assays to screen for compounds

that regulate the expression of genes associated with cholesterol

cas diagnostic indicators of cardiovascular disease and other disorders

can diagnostic indicators of cardiovascular disease and other disorders
   ó;
  Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
   131 agctctggccgctgccttccagggctcccgagccacacqctgggcgtgctggctgaggga 190
   0; Gaps
  /*tag= a
/product= "Human ABC1 protein, amino acids 1 to 60"
   Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
   21.6%; Score 77; DB 22; Length 10474; 99.2%; Pred. No. 4.8e-28;
  Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;
  1; Indels
  0; Mismatches
  Claim 30; Page 165-172; 211pp; English.
   associated with hypercholesterolemia.
   Location/Qualifiers
  Partial human ABC1 cDNA sequence.
  AAS04035 standard; cDNA; 446 BP.
   Oram JF,
   12-SEP-2001 (first entry)
  Best Local Similarity 99.29
Matches 127; Conservative
                             WPI; 2001-137811/14.
 Lawn RM, Wade D,
   atherosclerosis -
  251 gacaaaca 258
  381 gacaaaca 388
   P-PSDB; AAB31367
   WO200130848-A2
  Homo sapiens
  03-MAY-2001.
   Query Match
   AAS04035;
   6
   AAS04035
   Key
   RESULT
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  a
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```
Human; cytokine; cell proliferation; cell differentiation; growth factor;
  Naudin L;
   The sequence represents the partial coding sequence of human ABC1, which encodes amino acids 1-60 of the human ABC1 protein. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of coholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of coholesterol. The nucleic acids and polypeptides are also
   bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
antifungal; vulnerary; antiulcer; ss.
  Brewer HB;
   Gaps
   haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; athma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
  useful for treating and preventing cardiovascular and neurological pathologies, and other diseases e.g. Tangier disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
  0;
  Rosier-Montus M, Arnould-Reguigne I, Prades C,
Duverger N, Jaye M, Searfoss GH, Remaley A, B
   16.8%; Score 60; DB 22; Length 446; 100.0%; Pred. No. 1.1e-19; tive 0; Mismatches 0; Indels
  New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes
   Sequence 446 BP; 96 A; 123 C; 112 G; 115 T; 0 other;
  Human ABCAl homologue-encoding cDNA, SEQ ID NO:976.
  Example 2; Page 167; 368pp; English.
  ABA09200 standard; cDNA; 7086 BP.
                26-OCT-2000; 2000WO-EP10886.
  26-OCT-1999; 99EP-0402668.
01-MAR-2000; 2000US-0186260.
   (AVET ) AVENTIS PHARMA SA.
  Local Similarity 100.C
les 60; Conservative
  11-JAN-2002 (first entry)
   WPI; 2001-316327/33.
   P-PSDB; AAU02176
   WO200157188-A2.
   Homo sapiens.
  Denefle P,
Lemoine C,
  Query Match
   ABA09200;
  Dean M;
  Matches
  ABA09200
qq
```

```
Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides. Concleotide of the invention allowed of detecting the nucleotides or polypeptides of the invention and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may concentrate activities, and hence to potential therapeutic applications. The polypeptides of the invention may have various activities; stem cell growth factor activity; has receptor or information activities; concentration activities; concentration activities; concentration activities; on may be nead to activities; concentration are useful for preventing, treating or metastasis.

Conditions e.g., by protein or gene therapy. Such conditions include cancers, haematopotatic disorders (e.g., metopotatic activities and nucleotides of the invention are useful for preventing, treating or ameliorating medical carreial ischemma, bone disorders (e.g., metopotatic), athonic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischemma, bone disorders (e.g., metoporosis), and abnormal cracial schemma, bone disorders (e.g., metoporosis), and abnormal cracial inflammatory activities may be used to promote wound to muniopulatory activities may be used in the treatment of viral, munnomodulatory activities may be used in the treatment of viral, channed to promote cell growth factor activity may be used in cell culture to an individual properties the nealing (e.g., of burns, incisions and ulocars), while those with growth factor activity may be used
  autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
   Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
   that can be used to augment or replace cells damaged by illness,
  Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
  Claim 1; Page 833-835; 1963pp; English
   Tang YT, Liu C, Drmanac RT;
   05-FEB-2001; 2001WO-US03800.
  2000US-0496914
  27-APR-2000; 2000US-0560875
  e.g. arthritis and cancer -
  WPI; 2001-457740/49.
   (HYSE-) HYSEQ INC.
  P-PSDB; ABB11956
  03-FEB-2000;
09-AUG-2001
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Ouery Match 16.8%; Score 60; DB 22; Length 7086;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AAK52667 standard; cDNA; 7086 BP

RESULT 11 AAK52667 ID AAK5260

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   The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, harmatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
   Ma Y;
  Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
  0; Gaps
   Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
  Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Wang D, Wang J, Ren F, Chen R, Wang ZW; Yang Y, Wejhrman T, Goodrich R;
  Query Match 16.8%; Score 60; DB 22; Length 7086; Best Local Similarity 100.0%; Pred. No. 1.1e-19; Matches 60; Conservative 0; Mismatches 0; Indels
  Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
   Claim 1; Page 4558-4560; 6221pp; English.
   Human polynucleotide SEQ ID NO 2196.
  AAD21326 standard; DNA; 7260 BP.
  2000US-0620325.
2000US-0654936.
2000US-0663561.
  2000US-0560875
2000US-0598075
   20-OCT-2000; 2000US-0693325
30-NOV-2000; 2000US-0728422
   05-FEB-2001; 2001WO-US04098
  2000US-0496914
  (first entry)
   WPI; 2001-476283/51.
P-PSDB; AAM79534.
  (HYSE-) HYSEQ INC.
   WO200157190-A2.
   inflammation.
   3-FEB-2000;
  19-JUL-2000;
01-SEP-2000;
   15-SEP-2000;
   27-APR-2000;
  20-JUN-2000;
  06-NOV-2001
  09-AUG-2001
   OA,
   Tang YT,
             AAK52667;
   Xue AJ,
  RESULT 12
   AAD21326
ID AAD2
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Human; ATP binding cassette transporter 1; ABC1; coronary heart disease;
   The invention relates to four common polymorphisms in the gene encoding APP-binding cassette transporter-1 (ABC1). ABC1 is associated with decreased AppA-1 mediated efflux of cholesterol. The polymorphisms in ABC1 directly affects cellular lipid homeostasis, which is a key factor in the atherogenetic processes. The ABC1 polymorphisms are useful for diagnosing and treating lipid disorders, cardiovascular diseases (coronary heart disease, atherosclerosis) and inflammatory diseases (psortasis, lupus erythematosus). The identification of ABC1 as a transporter for interleukin-lbeta (IL-lbeta) identifies this gene as a candidate for treatment of inflammatory diseases including rheumatoid
   dermatological; atherosclerosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
  New adenosine triphosphate binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
  Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
   Human ATP binding cassette transporter 1 (ABC1) gene.
  /product= "Human ABC1 protein"
   Location/Qualifiers
321..7106
  Example 1; Fig 1; 48pp; English.
   20-MAR-2000; 2000EP-0105820
  20-MAR-2000; 2000EP-0105820
  28-JAN-2002 (first entry)
   /*tag=
  Schmitz G, Bodzioch M;
   WPI; 2001-640388/74.
  (FARB ) BAYER AG.
   P-PSDB; AAE13022.
  Homo sapiens
  EP1136552-A1
                  AAD21326;
```

arthritis and septic shock. The present sequence is human ABC1 gene. Length 7260; Score 60; DB 22; I Pred. No. 1.1e-19; ch 16.8%; Score 60; DB Similarity 100.0%; Pred. No. 1.1.60; Conservative 0; Mismatches Best Local Similarity Query Match

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0; Gaps
  Human ATP binding cassette transporter 1 (ABC1) cDNA.
  AAI70315 standard; cDNA; 7260 BP
   07-JAN-2002 (first entry)
   AAI70315
Matches
   RESULT 13
   AAI7031
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                                g
   DX LX S
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Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;

```
The present sequence is that of cDNA encoding the human adenosine triphosphate (ATP) binding cassette transporter 1 (ABC1) protein (see AMM5027). The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AAT70314, using an alternative ATG codon as initiation codon and thereby adding an extra 40 Nterminal amino acids to the encoded ABC1 protein (see AMM50228). The invention provides 4 common polymorphisms in the ABC1 gene. These were identified by sequencing the ABC1 gene in different Tangier kindreds. In the variant genes (numbering as in alternation 136, A is changed to G at position 5589 or G is changed to C at position 136, A is changed to G at position 2589 or G is changed to C at position 3456, or any combination of these. All of these polymorphisms alter the amino acid sequence of ABC1 and therefore may affect its function. The 2 most common polymorphisms (G596A) and A2589G are both associated with a decreased in vitro ApoA-I mediated efflux of cholesterol from mononuclear phagocytes, a cature typical of Tangier disease. 3 of the variants (G596A, A2589G and G3456C) are significantly increased in a population of manding low high density lipoprotein cholesterol lower.
  /*tag= b
/note= "alternative open reading frame of AAI70314"
  established coronary heart disease (CHD) relative to CHD-free control subjects. The use of the provided ABC1 polymorphisms for the diagnosis and treatment of lipid disorders, cardiovascular diseases, and inflammatory diseases (e.g. psoriasis, lupus erythematodes) is claimed. Modulation of ABC1 transcripts or proteins by antisense or ribozyme technology or RNA decoys is also
  New adenosine triphosphate binding cassette transporter gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
             ATP binding cassette transporter 1; ABC1; human; lipid disorder; cholesterol; cardiovascular disease; inflammatory disease; antiinflammatory; antilipeamic; antipsoriatic; dermatological; Tangier disease; coronary heart disease; diagnosis; gene therapy;
   Disclosure; Page 26-28; 41pp; English.
   Location/Qualifiers
   replace(1516,C)
   replace(2969,G)
  replace(3836,C)
  replace(976, A)
   24-MAR-2000; 2000EP-0106401
   24-MAR-2000; 2000EP-0106401
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   /*tag=
  /*tag=
  /*tag=
  Schmitz G, Bodzioch
   WPI; 2001-640389/74.
  polymorphism; ss.
  (FARB ) BAYER AG.
  P-PSDB; AAM50228
  Homo sapiens.
  EP1136554-A1
  26-SEP-2001.
  variation
   variation
   variation
  variation
   claimed.
   Key
   CDS
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ö
                       Gaps
                        .;
0
 Length 7260;
            1.1e-19;
nes 0; Indels
DB 22;
            1 Similarity 100.0%; Pred. No. 1.1
60; Conservative 0; Mismatches
  Score 60;
   16.8%;
    Query Match
                 Best Local
                           Matches
```

199 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 258 327 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 386 g ŏ

```
Human polynucleotide SEQ ID NO 228.
 AAK51683 standard; cDNA; 7281
        (first entry)
        06-NOV-2001
     AAK51683;
AAK51683
```

Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss. WO200157190-A2 Homo sapiens.

09-AUG-2001

2000us-0560875. 2000us-0598075. 2000us-0620325. 05-FEB-2001; 2001WO-US04098. 2000US-0496914. 27-APR-2000; 20-JUN-2000; 03-FEB-2000; 19-JUL-2000;

2000US-0728422 30-NOV-2000;

2000US-0654936. 2000US-0663561. 2000US-0693325.

01-SEP-2000; 15-SEP-2000; 20-OCT-2000; (HYSE-) HYSEQ INC.

Asundi V, Zhou P, Xu C, Cao Y, ang J, Ren F, Chen R, Wang ZW; Wang J, Zhang J, Ren Wejhrman T, Goodrich R; Drmanac RT, Liu C, Li Wang D, Yang Y, rang YT, OA,

Ma Y;

WPI; 2001-476283/51. P-PSDB; AAM78550.

Xue AJ,

Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy

Claim 1; Page 1086-1096; 6221pp; English.

The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAK9832-AAM80302) that exhibit activity elating to encoded polypeptides (AAK9832-AAM80302) that exhibit activity elating to eyotkine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.

Note: Records for SEO ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication. Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;

```
The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is notly two genetic HDL (high density lipoprotein) deficiency disorders, with two genetic HDL (high density lipoprotein) deficiency disorders, with two genetic HDL (high density lipoprotein) deficiency disorders, are distinguishable in that TD is an autosomal recessive disorder, while FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, coronary restenosis, and peripheral vascular disease.

Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and
                                  ö
  Human ABC1 cholesterol transporter; chromosome 9q31;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotein; rangler disease; TD; familial HDL deficiency; FHA; polymorphism; cardiovascular disease; coronary artery disease; coronary restenosis; cerebrovascular disease; peripheral vascular disease; Alzheimer's disease; huntington's disease; X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
   Human ABC1 cholesterol transporter FHA-3 mutant cDNA (delta 5752-5757).
   New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
                                    Gaps
                                    ;
0
Length 7281;
 16.8%; Score 60; DB 22; I
100.0%; Pred. No. 1.1e-19;
               100.0%; Prec. ....
   Hayden MR, Wilson AR, Pimstone SN;
  Examples; Page -; 229pp; English.
   AAC69388 standard; cDNA; 7857 BP
   (UYBR-) UNIV BRITISH COLUMBIA
  (XENO-) XENON BIORESEARCH INC
  99US-0138048.
99US-0139600.
99US-0151977.
  15-MAR-2000; 2000WO-IB00532.
   99US-0124702.
  (first entry)
  60; Conservative
  disease and cancer -
   WPI; 2000-587528/55.
                        Best Local Similarity
   P-PSDB; AAB38107
   WO200055318-A2.
   Homo sapiens.
   15-MAR-1999;
  08-JUN-1999;
   01-SEP-1999;
  29-JAN-2001
  21-SEP-2000
     Query Match
   12
  Matches
  AAC69388
  δλ
```

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ABC1 gene. Human ABC1 proteins disease, especially coronary artery disease, or prevent cardiovascular disease, especially coronary artery disease, or prevent cardiovascular disease, especially coronary artery disease, disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzhelmer's disease, Niemann-Pick disease, Huntingfon's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid acid with the exact sequence as GenBank Accession No: CAA10005.1 and X75926, and the nucleic present sequence represents convents as GenBank Accession No: AJ012376.1. The present sequence represents convents and an altered followed by a mutant human ABC1 cholesterol transporter associated with an altered followed and therefore an altered risk of cardiovascular disease.
   ö
  /note= "the coding sequence continues beyond nucleotide 3341, possibly till position 6860 as identified by translating the present sequence; part of the corresponding protein is missing and nucleotide 3341 corresponds to the last amino acid residue (position 1089) as indicated in the specification.
transgenic cells and non-human animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the
   0; Gaps
   but is
  ABC1; antilipemic; cholesterol; inhibitor; low density lipoprotein;
   Note: The present sequence is not shown in the specification, k
derived from the native human ABC1 cDNA shown on pages 157-160
  DB 21; Length 7857;
  Sequence 7857 BP; 2011 A; 1860 C; 2008 G; 1977 T; 1 other;
   0; Indels
   1.1e-19;
   /product- "partial ABC1 protein"
   Pred. No. 1.1 Mismatches
  16.8%; Score 60;
   Location/Qualifiers
   (WISC ) WISCONSIN ALUMNI RES FOUND.
  16.0°,
100.0%; Pre
0;
  AAF83826 standard; DNA; 7860 BP.
  Human ABC1 nucleotide sequence
  01-NOV-2000; 2000WO-US30109.
  30-JUN-2000; 2000US-0215564.
  99US-0162803
   (first entry)
   /*tag≈ a
   60; Conservative
   ..3341
   Best Local Similarity
Matches 60; Conserv
   WO200132184-A2.
  Homo sapiens.
   06-AUG-2001
  01-NOV-1999;
   10-MAY-2001
   AAF83826;
  Query Match
  LDL; ds.
  RESULT 16
  AAF83826
      888888888888888888888888888888888
   ò
  g
```

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The invention relates to a new method for inhibiting cholesterol uptake in the gut that comprises administration of an inhibitor of an ABC1 protein. The method is useful for: lowering levels of LDL (low density lipoprotein) cholesterol by reducing the activity of ABC1 protein in the intestinal cells and the abundance of the ABC1 protein in the individual by inhibiting the activity of the protein; identifying drugs that can lower serum cholesterol and LDL levels comprises assaying the drug to test if it can bind to an ABC1 protein; testing LDL cholesterol lowering agents; and for modulation of ABC1 biological activity. The present
  Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-
   High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABCl; ss.
   Gaps
   New method for inhibiting cholesterol uptake in the gut comprises
  The present invention relates to a method for treating a patient
  .
`
 Cook M, Gray-Keller MP, Hayden MR, Pimstone S;
  Length 7860;
  Sequence 7860 BP; 2013 A; 1861 C; 2009 G; 1977 T; 0 other;
  0; Indels
  sequence represents a human ABC1 nucleotide sequence.
   Clee SM;
   administration of an inhibitor of an ABC1 protein
   16.8%; Score 60; DB 22; I
100.0%; Pred. No. 1.1e-19;
iive 0; Mismatches 0;
  Hayden MR, Brooks-Wilson AR, Pimstone SN,
   or RXR-mediated transcriptional activity -
  Disclosure; Page 34-36; 41pp; English
   Disclosure; Fig 2; 317pp; English.
  AAF92835 standard; DNA; 7860 BP.
   (UYBR-) UNIV BRITISH COLUMBIA
  01-SEP-2000; 2000WO-IB01492.
  99US-0151977.
  2000US-0526193
   2000US-0213958
  17-MAY-2001 (first entry)
  (XENO-) XENON GENETICS INC
  60; Conservative
  2001-335779/35.
  Best Local Similarity
  WPI; 2001-244356/25.
Attie AD, Cook Brooks-Wilson A;
   P-PSDB; AAB62691
  Human ABC1 cDNA
   WO200115676-A2
  Homo sapiens.
   01-SEP-1999;
   23-JUN-2000;
   L5-MAR-2000;
   08-MAR-2001.
  AAF92835;
   Query Match
   Matches
   AAF92835
 g
  ò
```

```
The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is amember of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being
  ö
  Human ABC1 cholesterol transporter; chromosome 9q31;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
Tangter disease; TD; familial HDL deficiency; FHA; polymorphism;
cardiovascular disease; coronary artery disease; coronary restenosis;
cerebrovascular disease; peripheral vascular disease;
Allahamer's disease; Niemann-Pick disease; Huntington's disease;
X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
   selected a
   Human ABC1 cholesterol transporter FHA-1 mutant cDNA (delta 2151-2153)
   199 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 258
   New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
  Gaps
  ö
diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
   16.8%; Score 60; DB 22; Length 7860; 100.0%; Pred. No. 1.1e-19; tive 0; Mismatches 0; Indels v
  Sequence 7860 BP; 2014 A; 1860 C; 2008 G; 1978 T; 0 other;
   Hayden MR, Wilson AR, Pimstone SN;
  Examples; Page -; 229pp; English.
   AAC69387 standard; cDNA; 7861 BP
  UYBR-) UNIV BRITISH COLUMBIA
  (XENO-) XENON BIORESEARCH INC
  99US-0138048.
99US-0139600.
   15-MAR-2000; 2000WO-IB00532.
  99US-0124702.
   99US-0151977.
   (first entry)
  Conservative
  WPI; 2000-587528/55.
P-PSDB; AAB38106.
  Similarity
  disease and cancer
  WO200055318-A2
   Homo sapiens.
   01-SEP-1999;
  L5-MAR-1999;
   7-JUN-1999;
   29-JAN-2001
   21-SEP-2000.
   08-JUN-1999;
  903
  AAC69387;
   Query Match
Best Local S
  Matches
   AAC69387
   RESULT
  888888888888888
```

```
cc involved in cholesterol efflux from the cell. The gene encoding ABC1 is located on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, rangiter diseases (TD) and familial HDL deficiency (FHA). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease.

Cc cardiovascular disease. The invention provides genetic constructs and transgenic cells and non-human animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of acids, and methods of gene therapy for the treatment or prevention of acids, and methods of gene therapy for the treatment or prevention of acids, and methods of screening for such compounds which main. ABC1 per acidiovascular disease decivity, compounds which main. ABC1 acivity, compounds which corresponds which main. ABC1 activity, compounds which main. ABC1 activity, oncompasses compounds which main. ABC1 activity, once to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, disease, coronary restenosis or peripheral vascular disease, coronary restenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease. Huntington's disease, X-linked adrenoletwoystrophy and canoer. The invention specifically excludes proteins and methods of sequences of Genbank Accession No: CAALO005.1 and X75926, and the nucleic acid with the exact sequence as Genbank Accession No: CAALO005.1 and X75926, and the nucleic represents compared where the devact sequences as Genbank Accession No: CAALO005.
  transporter associated with an altered cholesterol level and therefore an altered risk of cardiovascular disease.
  Human ABC1 cholesterol transporter; chromosome 9931;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotein; Tangier disease; TD; familial HDL deficiency; FHA; polymorphism; cardiovascular disease; coronary artery disease; coronary restenosis;
   X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prognosis; prophylaxis; drug screening; transgenic animal; ss.
  199 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 258
  Note: The present sequence is not shown in the specification, but is derived from the native human ABC1 cDNA shown on pages 157\text{-}160.
   0; Gaps
   cerebrovascular disease; peripheral vascular disease;
Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
  16.8%; Score 60; DB 21; Length 7861;
  Sequence 7861 BP; 2014 A; 1859 C; 2011 G; 1976 T; 1 other;
  Indels
   1.1e-19;
hes 0;
  100.0%; Pred. w. +ive 0; Mismatches
   Human ABC1 cholesterol transporter cDNA.
   AAC69120 standard; cDNA; 7864 BP
  15-MAR-2000; 2000WO-IB00532.
  29-JAN-2001 (first entry)
   Conservative
   Query Match
Best Local Similarity
  WO200055318-A2.
   21-SEP-2000.
  90;
   AAC69120;
  19
   Matches
   RESULT
   g
                          οy
```

```
The invention relates to the human ABCI cholesterol transporter protein (838082) and to nucleic acid sequences (C69120) which encode it. ABCI is a member of the ATP-binding cassette (ABC transporter) superfamily of a member of the ATP-binding cassette (ABC transporter) superfamily of intracellular cholesterol trafficking in monocytes and fibroblasts, being to convert the color trafficking in monocytes and fibroblasts, being involved in cholesterol trafficking in monocytes and fibroblasts, being concered on chromosome 9431, and mutations in this gene encoding ABCI is with two genetic HDL (high density lipoprotein) deficiency disorders.

CC action on chromosome 9431, and mutations in this gene are associated and in the tropic of a interest of the color of an expectation of the blood correlate with a high risk of cardiovascular closesterol') in the blood correlate with a high risk of cardiovascular closeses. Particularly coronary artery disease, but also cerebrovascular closeses. Particularly coronary artery disease, but also cerebrovascular closeses. Particularly coronary artery disease, but also cerebrovascular cardiovascular disease. The invention provides genetic constructs and cardiovascular disease compounds which mained ABCI the treatment or prevention of cardiovascular disease comprising the administration of merphesis of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of merphesis of gene therapy for the treatment of cardiovascular disease comprising the administration of merphesis of genetheds for determining whether a patient has an ABCI gene. Human ABCI proteins and methods of screening for such compounds to increased risk for cardiovascular disease, especially coronary artery disease, selective or prevent cardiovascular disease, coronary restenois or periphory and contract or prevent cardiovascular disease, coronary restenois or periphory and contract or prevent cardiovascular disease, selecting contract and nethods of cardiovascular diseases. They 
  The invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic acid with the exact sequence as GenBank Accession No: AJ012376.1. The
  New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
   present sequence represents cDNA encoding the human ABC1 cholesterol
  Claim 13; Page 157-160; 229pp; English.
  Hayden MR, Wilson AR, Pimstone SN;
   BRITISH COLUMBIA.
  (XENO-) XENON BIORESEARCH INC.
                               99US-0138048.
99US-0139600.
  99US-0151977.
       99US-0124702.
   disease and cancer -
  WPI; 2000-587528/55.
   P-PSDB; AAB38082.
  15-MAR-1999;
08-JUN-1999;
17-JUN-1999;
   UYBR-) UNIV
  01-SEP-1999;
```

Sequence 7864 BP; 2014 A; 1860 C; 2011 G; 1978 T; 1 other;

```
ö
                            0; Gaps
16.8%; Score 60; DB 21; Length 7864;
                0; Indels
          1.1e-19;
    100.0%; Preq. ....
                Conservative
       Similarity
Query Match
Best Local Simi
Matches 60;
                              ò
  Ω
```

```
AAC69385 standard; cDNA; 7864 BP
   AAC69385;
RESULT 20
               AAC69385
```

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Human ABC1 cholesterol transporter; chromosome 9q31; ATP-binding casette; HDL deficiency disorder; hIgh density lipoprotein; Tangler disease; TD; familial HDL deficiency; FHA; polymorphism; cardiovascular disease; coronary artery disease; coronary restenosis; cerebrovascular disease; peripheral vascular disease; standard disease; huntington's disease; X-linked darenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
                 Human ABC1 cholesterol transporter TD-1 mutant cDNA (T4503C).
   Pimstone SN;
  (UYBR-) UNIV BRITISH COLUMBIA
   (XENO-) XENON BIORESEARCH INC
  99US-0138048.
   99US-0151977.
  15-MAR-2000; 2000WO-IB00532.
  99US-0124702
29-JAN-2001 (first entry)
  Hayden MR, Wilson AR,
  WPI; 2000-587528/55.
  P-PSDB; AAB38104.
   WO200055318-A2.
  15-MAR-1999;
   08-JUN-1999;
  01-SEP-1999;
  21-SEP-2000.
```

New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's disease and cancer -

Examples; Page -; 229pp; English.

The invention relates to the human ABC1 cholesterol transporter protein

(B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
a member of the ATP-binding cassette (ABC transporter) superfamily of
proteins, and plays a crucial role in cholesterol transport, particularly
intracellular cholesterol trafficking in monocytes and fibroblasts, being
cocated on cholesterol trafficking in monocytes and fibroblasts, being
involved in rohlesterol efflux from the cell. The gene encoding ABC1 is
cocated on chromosome 9931, and mutations in this gene are associated
with two genetic HDL (high density lipoprotein) deficiency disorders,
are distinguishable in that TD is an autosomal recessive disorder, while
FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
closesterol") in the blood correlate with a high risk of cardiovascular
disease, particularly coronary artery disease, but also cerebrovascular
disease, coronary restenosis, and peripheral vascular disease.
Conversely, a high level of HDL has protective effects against
cardiovascular disease. The invention provides genetic constructs and
transconic collises. cerebrovascular disease, coronary restenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABCI biological activity, such as Alzheimer's disease, Niemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic acid with the exact sequence as GenBank Accession No: AJ012376.1. The transgenic cells and non-luman animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which mimic ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease,

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The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is located on chromosome 9931, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
   ;
0
present sequence represents CDNA encoding a mutant human ABC1 cholesterol transporter associated with an altered cholesterol level and therefore an altered fisk of carditovascular disease.

Note: The present sequence is not shown in the specification, but is derived from the native human ABC1 cDNA shown on pages 157-160.
  Human ABC1 cholesterol transporter; chromosome 9931;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
  cerebrovascular disease; peripheral vascular disease;
Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
   cardiovascular disease; coronary artery disease; coronary restenosis;
  Gaps
  New ABC1 polypeptide is useful for treating diseases associated v
ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
  ö
  Human ABC1 cholesterol transporter TD-2 mutant cDNA (A1864G).
   16.8%; Score 60; DB 21; Length 7864; 100.0%; Pred. No. 1.1e-19; ive 0; Mismatches 0; Indels
   Sequence 7864 BP; 2014 A; 1861 C; 2011 G; 1977 T; 1 other;
   Pimstone SN;
   Examples; Page -; 229pp; English.
  AAC69386 standard; cDNA; 7864 BP
  UNIV BRITISH COLUMBIA.
   XENO-) XENON BIORESEARCH INC
   99US-0124702.
  99US-0138048.
  99US-0151977.
   15-MAR-2000; 2000WO-IB00532.
  29-JAN-2001 (first entry)
  60; Conservative
   Hayden MR, Wilson AR,
   WPI; 2000-587528/55.
   Best Local Similarity
  disease and cancer
  P-PSDB; AAB38105.
   WO200055318-A2.
   Homo sapiens.
   15-MAR-1999;
   21-SEP-2000.
  08-JUN-1999;
  01-SEP-1999;
  AAC69386;
  Query Match
  UYBR-)
  Matches
   AAC69386
   RESULT
   á
  g
           8
```

```
cc are distinguishable in that TD is an autosomal recessive disorder, while CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease.

C conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and transgenic cells and non-human animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising tragment thereof. The invention also cencompasses compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat corpusated risease, coronary restenosis or peripheral vascular cardiovascular disease, especially coronary artery disease, cerebrovascular disease, especially coronary artery disease, with ABC1 biological activity, such as Alzheimer's disease, Niemann Pick disease, Huntington's disease, Alianked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CAAl0005.1 and X75926, and the nucleic cardiovascular conversents convary artery human ABC1 charactery corpus more as GenBank Accession No: ADA12376.1. The cardiovascular charactery convary artery human ABC1 charactery conversed to the part of the pa
   ó
  present sequence represents cDNA encoding a mutant human ABC1 cholesterol transporter associated with an altered cholesterol level and therefore an
  Human ABC1 cholesterol transporter; chromosome 9q31;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
Tangler disease; TD; familial HDL deficiency; FHA; polymorphism;
cardiovascular disease; coronary artery disease; coronary restenosis;
cerebrovascular disease; peripheral vascular disease;
Albahaner's disease; Niemann-Pick disease; Huntington's disease;
X-linked adrenoleukodystrophy, cancer; gene therapy; genetic diagnosis;
prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
  0; Gaps
  Note: The present sequence is not shown in the specification, but is derived from the native human ABC1 cDNA shown on pages 157\text{-}160.
  Human ABC1 cholesterol transporter FHA-2 mutant cDNA (C6504T).
   Query Match 16.8%; Score 60; DB 21; Length 7864; Best Local Similarity 100.0%; Pred. No. 1.1e-19; Matches 60; Conservative 0; Mismatches 0; Indels 0
  Sequence 7864 BP; 2013 A; 1860 C; 2012 G; 1978 T; 1 other;
  altered risk of cardiovascular disease.
  AAC69389 standard; cDNA; 7864 BP.
  99US-0138048.
99US-0139600.
99US-0151977.
   99US-0124702.
   15-MAR-2000; 2000WO-IB00532
  29-JAN-2001 (first entry)
  WO200055318-A2.
  08-JUN-1999;
17-JUN-1999;
01-SEP-1999;
  Homo sapiens.
  15-MAR-1999;
  21-SEP-2000,
  AAC69389;
   RESULT 22
   AAC69389
  δλ
                               8588888888888888888888888888888888888
```

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The invention relates to the human ABCI cholesterol transporter protein (183802) and to nucleic acid sequences (C69120) which encode it. ABCI is a member of the ATP-binding cassette (ABC transporter) specifically of proteins, and plays a crucial role in cholesterol transport, particularly citransporter support, particularly citransporter particularly citransporter and fibroblasts being involved in cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABCI is involved in cholesterol efflux from the cell. The gene encoding ABCI is with two genetic HDL (high density lipoprotein) deficiency disorders, with two genetic HDL (high density lipoprotein) deficiency (FMA). These diseases of the at distanguishable in that TDL is an autosomal recessive disorder, while conclusion that TDL is an autosomal recessive disorder, while the and stationushable in that TDL is an autosomal recessive disease. Coronary restenosis, and peripheral vascular disease. Oronary restenosis, and peripheral vascular disease. Coronary restenosis, and provention provides genetic constructs and cardiovascular disease. The invention provides genetic constructs and cardiovascular disease comprising the administration of an expression encompasses compounds which mimic ABCI attrict, cardiovascular disease, coronary restenosis, and methods of screening for such compounds to receive the relates to methods for determining whether a patient has an increased risk for cardiovascular disease, coronary restenosis or peripheral vascular disease. Coronary restenosis or peripheral vascular disease, coronary restenosis with ABCI biological activity, such as Alzheimer's disease, and th
  New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
   Hayden MR, Wilson AR, Pimstone SN;
  Examples; Page -; 229pp; English.
                      (UYBR-) UNIV BRITISH COLUMBIA. (XENO-) XENON BIORESEARCH INC.
  disease and cancer -
  WPI; 2000-587528/55.
   P-PSDB; AAB38108
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0; Gaps
Note: The present sequence is not shown in the specification, but is derived from the native human ABC1 cDNA shown on pages 157-160.
   16.8%; Score 60; DB 21; Length 7864;
   0; Indels
   Sequence 7864 BP; 2014 A; 1859 C; 2011 G; 1979 T; 1 other;
  1.1e-19;
  100.0%; Pred. No. 1.1 cive 0; Mismatches
  Best Local Similarity 100.(
Matches 60; Conservative
   Query Match
```

```
AAS06120 standard; cDNA; 9741 BP.
  12-SEP-2001 (first entry)
  AAS06120;
   RESULT 23
   AAS06120
δλ
                 qq
```

```
The sequence represents the coding sequence #1 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dystunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological pathologies, and other diseases e.g. Tangyler disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
  Naudin L;
   s M, Arnould-Reguigne I, Prades C, Naudin L,
Jaye M, Searfoss GH, Remaley A, Brewer HB;
   0; Gaps
   Human, ABC1 gene; atherosclerosis; reverse transport; cholesterol;
cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
  Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
cardiovascular; neurological; Tangler disease;, LCAT deficiency;
   16.8%; Score 60; DB 22; Length 9741; 100.0%; Pred. No. 1.1e-19; tive 0; Mismatches 0; Indels (
   New human ABC1 nucleic acids and polypeptides for treating
  Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;
  /*tag= a
/product= "Human ABC1 protein"
   atherosclerosis, malaria and diabetes
  Claim 1; Page 204-208; 368pp; English.
  Location/Qualifiers
   AAS06121 standard; cDNA; 9854 BP.
  26-OCT-2000; 2000WO-EP10886.
  26-OCT-1999; 99EP-0402668.
01-MAR-2000; 2000US-0186260.
   Rosier-Montus M,
                Human ABC1 DNA sequence #1.
   (AVET ) AVENTIS PHARMA SA.
  Human ABC1 DNA sequence #2.
   Query Match
Best Local Similarity 100.09
   185..6967
   12-SEP-2001 (first entry)
  Duverger N,
  /*tag=
  WPI; 2001-316327/33.
   P-PSDB; AAU02176
   WO200130848-A2,
  Homo sapiens.
  03-MAY-2001.
  Denefle P,
Lemoine C,
  AAS06121;
   Dean M;
  RESULT 24
  AAS06121
op
   δλ
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  The sequence represents the coding sequence #2 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treatming and preventing actions cardiac and neurological pathologies, and other diseases e.g. Tangier disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
  detection; diagnosis; antisense therapy; gene therapy; ss.
  Naudin L;
   Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L
Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
   0; Gaps
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
  Length 9854;
   New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes -
  Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;
   Indels
   Match 16.8%; Score 60; DB 22; Lu
Local Similarity 100.0%; Pred. No. 1.1e-19;
les 60; Conservative 0; Mismatches 0;
  /product= "Human ABC1 protein"
   Human cDNA clone (5'-primer) SEQ ID NO:4267.
   Claim 1; Page 209-213; 368pp; English
  Location/Qualifiers 298..7078
  AAH07432 standard; cDNA; 736 BP
  26-OCT-2000; 2000WO-EP10886
  99EP-0402668
   01-MAR-2000; 2000US-0186260
   (first entry)
  (AVET ) AVENTIS PHARMA SA.
   /*tag=
   WPI; 2001-316327/33.
P-PSDB; AAU02176.
  Human; primer;
  WO200130848-A2
  EP1074617-A2
                               Homo sapiens
   26-JUN-2001
  26-OCT-1999;
  07-FEB-2001
   Denefle P,
Lemoine C,
   AAH07432;
  Query Match
  Dean M;
  Matches
  ŏ
   q
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the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13628 and AAH13633 to AAH13628 and AAH13633 to AAH13639 to AAH13632 represent human anino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
  The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligoral primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence.
  Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
  Gaps
  Yamamoto J;
  ö
   14.3%; Score 51; DB 22; Length 736; 100.0%; Pred. No. 2.9e-15; tive 0; Mismatches 0; Indels
  Saito K, Ya
, Otsuki T;
  Sequence 736 BP; 163 A; 199 C; 199 G; 170 T; 5 other;
  Claim 1; SEQ ID 4267; 2537pp + CD ROM; English
  Isogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
   Human cDNA sequence SEQ ID NO:18808
   AAH18606 standard; cDNA; 1556
   99JP-0248036.
  11-JAN-2000; 2000JP-0118776
             28-JUL-2000; 2000EP-0116126
  02-MAY-2000; 2000JP-0183767
09-JUN-2000; 2000JP-0241899
  51; Conservative
  of the present invention.
  (HELI-) HELIX RES INST
   WPI; 2001-318749/34.
  Best_Local Similarity
Matches 51; Conserv
   full-length cDNAs
   Homo sapiens
   EP1074617-A2
  27-AUG-1999;
  26-JUN-2001
  AAH18606;
   Ishii S,
   Query Match
   AAH18606
   ò
   qq
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ö
  sequence and an oligonic lectified comprising a sequence complementary to a polynuclectide which comprises a 3' end sequence, where the polynuclectide which comprises a 1' end sequence, where the combination of the 5'-end sequence, 3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length convas. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length convas allow obtaining of the full-length convas an encoded in the full-length convas and methods. AAH13618 to AAH13628 and AAH13631 and AAH13631 converse and an and converse and and converse and an and an analysis of the abnormal converse and an analysis of the full-length converse and the analysis of the full-length and any specialised methods. AAH3618 for AAH13628 and AAH13631 and AAH1363
  AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
  The present invention describes primer sets for synthesising 5602 full-length cDMAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
   High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
   Gaps
  Yamamoto J;
   ö
  Length 1556;
  Saito K, Ya
Otsuki T;
  Indels
  Sequence 1556 BP; 380 A; 363 C; 399 G; 414 T; 0 other;
   14.3%; Score 51; DB 22; Lv
100.0%; Pred. No. 2.9e-15;
  Claim 8; SEQ ID 18808; 2537pp + CD ROM; English.
   sogai T, Nishikawa T, Hayashi K, S:
Sugiyama T, Wakamatsu A, Nagai K,
  ABC1 polymorphism RFLP oligionucleotide #45.
  99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
  AAF93084 standard; DNA; 37 BP
   28-JUL-2000; 2000EP-0116126
   17-MAY-2001 (first entry)
   Best_Local Similarity 100.0
Matches 51; Conservative
   of the present invention.
   (HELI-) HELIX RES INST.
  WPI; 2001-318749/34.
   Isoqai T,
  full-length cDNAs
   27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
  29-JUL-1999;
   09-JUN-2000;
  Homo sapiens
                             07-FEB-2001
   Ishii S,
   AAF93084;
   Query Match
   ota
g
   ò
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The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density ilpoprotean-cholesterol (ML-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates IXR- or RXR-mediated transcriptional activity or ABG1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
   Treating a lower than normal high density lipoprotein-cholesterol (HDL-0) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity
  High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
  Gaps
  ;
0
  Length 37;
  Indels
  Clee SM;
  ;
0
  2.1e-07;
   Score 35; DB 22;
Pred. No. 2.1e-07
   Sequence 37 BP; 4 A; 17 C; 11 G; 5 T; 0 other;
   138 gccgctgccttccagggctcccgagccacacgctg 172
  ABC1 polymorphism RFLP oligionucleotide #43.
  Hayden MR, Brooks-Wilson AR, Pimstone SN,
  100.08; Pred. ...
  1 geogetgeetteeagggeteecgageeacaegetg 35
   Disclosure; Fig 17; 317pp; English.
   (UYBR-) UNIV BRITISH COLUMBIA
   AAF93082 standard; DNA; 38 BP.
   (UYBR-) UNIV BRITISH COLUMBIA.
  15-MAR-2000; 2000US-0526193. 23-JUN-2000; 2000US-0213958.
  9.88;
  01-SEP-2000; 2000WO-IB01492.
  2000US-0526193.
2000US-0213958.
   01-SEP-2000; 2000WO-IB01492.
   99US-0151977
  (XENO-) XENON GENETICS INC
  Query Match
Best Local Similarity 100.v
  17-MAY-2001 (first entry)
   WPI; 2001-244356/25.
           WO200115676-A2.
   WO200115676-A2.
  01-SEP-1999;
  15-MAR-2000;
23-JUN-2000;
  Homo sapiens
   01-SEP-1999;
                                      08-MAR-2001
  08-MAR-2001.
   AAF93082;
  AAF93082
   RESULT
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   δ
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Homo sapiens.
   W09957145-A2.
   Synthetic
  RESULT 30
  AAZ39175
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   The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
   Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-
   Gaps
  Low density lipoprotein binding protein 2; LBP-2; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis;
   ó
   Human low density lipoprotein binding protein 2 (LBP-2) gene.
  Length 38;
   0; Indels
                  Pimstone SN, Clee SM;
  % Match 9.8%; Score 35; DB 22; 1 Local Similarity 100.0%; Pred. No. 2.1e-07; nes 35; Conservative 0; Mismatches 0;
   Sequence 38 BP; 6 A; 15 C; 5 G; 12 T; 0 other;
   78 ccctcctgctttatctttcagttaatgaccagcc 112
  1 ccctcctgctttatctttcagttaatgaccagcc 35
  ′*tag= a
'note= "includes introns"
   or RXR-mediated transcriptional activity
   Location/Qualifiers
2832..5153
/*tag= a
   Disclosure; Fig 17; 317pp; English.
   AAH26495 standard; DNA; 12425 BP
                   Hayden MR, Brooks-Wilson AR,
  /*tag= i
4995..5153
  a d . 4899
  .4502
   ..3785
  .4593
   3= е
.4694
  .4787
  /*tag= b
3786..4207
   ..4994
   12-NOV-2001 (first entry)
(XENO-) XENON GENETICS INC
  /*tag=
  /*tag=
4900..4
   /*tag=
4788..4
   /*tag=
4594..4
  *tag=
  /*tag=
  4503
  1695
                                     WPI; 2001-244356/25
   Homo sapiens.
   vaccine; ds.
   AAH26495;
   Query Match
   intron
  intron
   intron
   intron
   exon
  exon
  exon
  exon
  exon
   Matches
   AAH26495
  RESULT
   Dp
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bone disease; osteohyperplasia; osteometastasis; orthopaedic surgery; osteoarthritis; arthrostelitis; tumour dissection; bone reconstruction; osteoarthritis; arthrostelitis; tumour dissection; bone reconstruction; ospinal fusion; vertebral canal enlargement; congenital cartilage disease; dysoteogenesis; achondroplasia; palatloschisis; mandible reconstruction; residual ridge construction; osteoporosis; morphogenesis; hyperplasia;
   The present sequence is that of genomic DNA encoding novel human conversity lipoprotein binding protein 2 (LBP-2, see AAB82806).

The DNA was isolated from a human genomic library by screening with LBP-2 DNA (see AAH82494). The open reading frame spans 5 exons. Human LBP-2 nucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides, termed LBPs, capable of inding to native and methylated LDL. Also claimed are isolated LBP propeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk or atherosclerosis, methods for treating an agent for use in abnormality in structure or metabolism of LBP are claimed.

The properties of the methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed.
  New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis
  Gaps
  Human BMP-4 5' upstream gene sequence with exon 1-3 PCR primer #1.
  Human; bone morphogenetic protein 4; BMP-4; promoter; cartilage;
  0;
  6.7%; Score 24; DB 22; Length 12425; 100.0%; Pred. No. 0.054; Live 0; Mismatches 0; Indels 0;
  Sequence 12425 BP; 2563 A; 3702 C; 3566 G; 2594 T; 0 other;
  nucleic acid, and vaccine compositions, are also claimed.
  Law SW, Arjona AA;
   2395 ggaggagggagggagggaaggaag 2418
   326 ggaggaggaggagggaaggaag 349
  Example 4; Fig 23; 143pp; English.
  (BOST-) BOSTON HEART FOUND INC.
   AAZ39175 standard; DNA; 30 BP
  02-MAR-2000; 2000US-0517849.
14-JUL-2000; 2000US-0616289.
  28-FEB-2001; 2001WO-US06356
  06-MAR-2000 (first entry)
   Best Local Similarity 100.
Matches 24; Conservative
/*tag=
   WPI; 2001-565505/63.
   Lees RS,
  P-PSDB; AAB82806
  PCR primer; ss.
  WO200164874-A2
  07-SEP-2001
   AAZ39175;
   Lees AM,
  Query Match
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The present sequence represents a PCR primer for the 5' upstream gene sequence including the exon 1 through exon 3 regions of human bone corphogenetic protein 4 (BMP-4). This region of DNA and a reporter gene morphogenetic protein 4 (BMP-4). This region of DNA and a reporter gene weight compounds which regulate the expression of human BMP-4. The low cartivity and inhibiting activity for bone and cartiales through the extression of human BMP-4, and are useful as preventative or therapeutic expression of human BMP-4, and are useful as preventative or therapeutic expression of human BMP-4, and are useful as preventative or therapeutic genetic for cartialge and bone diseases, and osteohyperplasia, and as remedies for osteometastasis. The compounds are also useful in the fields of orthopaedic surgery (fracture, osteoarthritis such as joint and hip joint osteoarthritis, atthrostelis, danage of cartilage such as damage of meniscus, regeneration of bone and cartilage deficit caused by injury and tumour dissection, bone reconstruction such as spinal compounds way also be used for bone graft in aesthetic surgery. The compounds also have application in the veterinary field. Those compounds that inhibit bone or cartilage morphogenesis are used for prevention and the rarrian and cartilage morphogenesis.
   .Ow molecular weight compounds which regulate the expression of BMP-4
   Human bone morphogenetic protein 4 (BMP-4) promoter used to identify
   Sequence 30 BP; 9 A; 2 C; 19 G; 0 U; 0 other;
   therapy of bone and cartilage hyperplasia.
  (HMRI ) HOECHST MARION ROUSSEL LTD.
   Example 1; Page 23; 23pp; English.
  AAC83229 standard; DNA; 1077 BP.
   326 ggaggaggagggaggaagga 347
   7 ggaggaggaggaaggaagga 28
  99WO-IB00732.
  98JP-0120173
   22; Conservative
   Kawai S, Sugiura T;
  WPI; 2000-062142/05
   Best Local Similarity
  22-APR-1999;
  30-APR-1998;
                        11-NOV-1999
   Query Match
  AAC83229
   Matches
```

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Gaps
   DNA sequence from the promoter region upstream of the See2a gene #2.
   Senescence; transgenic plant; promoter; transcription initiation; plant development; fruit ripening; protease inhibitor; pesticide; silage proteolysis inhibition; See2a; ds.
                             ;
6.2%; Score 22; DB 21; Length 30;
100.0%; Pred. No. 0.52;
tive 0; Mismatches 0; Indels
   13-MAR-2001 (first entry)
  WO200070061-A2.
  23-NOV-2000
  AAC83229/c
   ð
  g
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This invention relates to a promoter or transcriptional initiation
region of a plant genome that is capable of modifying gene expression
during plant material senescence. Plant senescence is the sequence of
during plant material senescence. Plant senescence is the sequence of
blochemical and physiological events comprising the final stage of plant
development. The promoter or a DNA construct containing the promoter is
useful for modifying gene expression during senescence, for delaying
senescence characteristics, and for modifying the expression of strong
also be used for the expression of antisense or senes protease sequences,
delaying fruit ripening, enhancing senescence characteristics of plant
material, modifying expression of at least 1 plant growth regulator, for
transforming plant material with a transgene under the control of the
promoter, for modifying expression of a protease inhibitor, pesticidal
ce promoter, for modifying expression of a protease inhibitor, pesticidal
content and DNA construct are also useful for producting a plant
material having modified gene expression during senescence for enhancing
the expression of pesticidal compounds during senescence, and for
the expression of pesticidal compounds during senescence, and for
the expression of metanishing the promoter or a construct and plant material with
the promoter or a construct are also useful for producing a plant
material having modified gene expression during senescence, and for
the expression of pesticidal compounds during senescence, and for
the expression or a construct are also useful for producing a plant
the normander or a construct and plant material with
   the promoter or a construct containing it. The present sequence represents a second variant of DNA from the promoter region upstream of the senescence-enhanced See2a gene isolated from Zea mays. This sequence
   modification of gene expression during senescence of plant material and for modifying expression of protease inhibitors and pesticidal genes -
   Gaps
   promoter; bone morphogenetic protein-4; BMP-4; estrogen receptor; osteoporosis; antitumour agent ICII64384; breast cancer; oestrogen;
   ö
  Promoter or DNA construct isolated from maize, useful in the
  6.2%; Score 22; DB 22; Length 1077; 100.0%; Pred. No. 0.52; Ve 0; Mismatches 0; Indels (
   Sequence 1077 BP; 328 A; 255 C; 236 G; 258 T; 0 other;
   can be used as the promoter region of the invention.
   Robson PRH, Griffiths CM;
  /*tag= a
/note= "Transcription start site"
1442..1456
/*tag= b
   (GRAS-) INST GRASSLAND & ENVIRONMENTAL RES.
   Location/Qualifiers
  1070 GGAGGGAGGGAAGCAAGC 1049
  Claim 1; Page 63; 66pp; English.
   100.0%; Pritive 0;
   AAV32783 standard; DNA; 1456 BP.
  329 ggagggagggagggaagc 350
  Human BMP-4 promoter region 1.
15-MAY-2000; 2000WO-GB01849.
  15-MAY-1999; 99GB-0011247.
   07-OCT-1998 (first entry)
  22; Conservative
   Thomas H, Donnison IS,
   endometrial cancer; ss.
   WPI; 2001-025023/03.
   Best Local Similarity
   Homo sapiens
  Key
misc_signal
   Query Match
   AAV32783;
  intron
   RESULT 32
  Matches
   AAV32783
  ò
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The sequences given in AAQ32850-56 encode bone morphogenetic proteins (BMP). BMP's increase bone growth and when used in conjunction with vitamin D the level of new bone growth is greater than when a BMP or vitamin D are used alone. The BMP's are administered for systemic treatment at a dose range of 1pg to 100 microg. BMP are active as
   Synergistic compsn. for generating mammalian bone growth comprises vitamin=D cpd. and bone morphogenetic protein
   Sequence 1751 BP; 394 A; 510 C; 490 G; 357 T; 0 other;
  Query Match 6.2%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 0.5 Matches 22; Conservative 0; Mismatches
  Disclosure; Page 31-32; 44pp; English.
  Claim 1; Column 23-24; 18pp; English.
            91US-0709621.
92US-0856110.
   (PROC ) PROCTER & GAMBLE CO
  WPI; 1998-031788/03.
  WPI; 1992-433371/52
   Unidentified
   05-JUN-1991;
   rickets; ds.
  US5693615-A.
  07-SEP-1993;
  05-JUN-1991;
27-MAR-1992;
  23-JAN-1995;
   02-DEC-1997.
   09-DEC-1992;
              05-JUN-1991;
                                  27-MAR-1992;
   Stone RL;
  AAV01680;
   Stone RL;
   34
   AAV01680
  The present sequence represents a human bone morphogenetic protein-4 promoter (BMP-4) region 1. The invention provides a method for the identification of therapeutic agents for use in the prevention and/or treatment of osteoporosis. The method involves introducing two expression vectors into a host cell. The first expression vector comprises of a BMP-4 promoter region 1 or 2 (AAV32784) which is operably intended to a reporter gene, e.g. BMP-4 gene. The second expression vector comprises of a DNA encoding an estrogen receptor. The host cell is then contacted with the compounds being being tested for therapeutic activity. Compounds which bind and form a complex with the estrogen receptor, to gain entry into the cell, and then induce the expression of the reporter gene, through the BMP-4 promoter region, are potential therapeutic candidates. By this method, the antitumour agent ICII64384 was shown to be an effective therapeutic agent. Unlike oestrogens currently used to treat osteoporosis, the therapeutic agents are claimed not to have an increment in the risk of developing breast or endometrial
   ;
0
   Gaps
   Promoter from human bone morphogenetic protein-4 gene - and related vectors and transformed cells, useful for screening agents for the treatment of osteoporosis
   Bone; morphogenetic; protein; BMP; growth; vitamin D; systemic;
   ;
  6.2%; Score 22; DB 19; Length 1456; 100.0%; Pred. No. 0.52;
   0; Indels
   Sequence 1456 BP; 357 A; 361 C; 410 G; 328 T; 0 other;
                    /note= "Partial intron sequence"
   0; Mismatches
  AAQ32853 standard; cDNA; 1751 BP
  1187 ggaggagggagggaggaagga 1208
  326 ggaggagggagggaggaagga 347
   Claim 2; Fig 5a; 41pp; English.
  Dijkema R, Van Den Wijngaard
  92WO-US04356
   96EP-0203283.
  97WO-EP06668
   05-MAY-1993 (first entry)
  Query Match
Best Local Similarity 100.C
Matches 22; Conservative
      /number= 1
   (ALKU ) AKZO NOBEL NV
   treatment; dimer; ss
   WPI; 1998-322720/28.
  Rattus rattus
  26-MAY-1992;
   10-DEC-1992
  20-NOV-1997;
   22-NOV-1996;
   WO9823740-A1
   04-JUN-1998
   AAQ32853;
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Gaps
   0;
  Bone morphogenetic protein; BMP; growth; vitamin D; fracture; arthritis; surgical lesion; periodontal disease; osteoporosis;
6.2%; Score 22; DB 13; Length 1751;
100.0%; Pred. No. 0.52;
   Generation of new bone growth – by co-administering bone morphogenetic protein and vitamin \boldsymbol{D}
   Indels
   ;
0
   Bone morphogenetic protein BMP-4 encoding DNA.
   AAV01680 standard; cDNA; 1751 BP
   326 ggaggaggagggaggaagga 347
   91US-0709621.
92US-0856110.
  92US-0988363
  91us-0709621
   93US-0117367
  94US-0243435
95US-0377292
   (PROC ) PROCTER & GAMBLE CO
  27-MAR-1998 (first entry)
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mammal. The method comprises administering a bone morphogenetic protein in combination with a vitamin D compound, where: (a) the bone morphogenetic protein is BMP-2 and is administered in an amount of 500-1000 ng in combination with about 6 ng vitamin D compound; or (b) the bone morphogenetic protein is BMP-4 and is administered in an amount of about 62.5 ng in combination with about 6 ng vitamin D compound; or (b) the present sequence encodes BMP-4. The method is used for treating bone defects or disorders, e.g. fractures, surgical lesions, periodontal disease, osteoporosis, arthritis and rickets.
   Gaps
           method has been developed for generating new bone growth in a
   ;
0
   Osteogenic protein; bone; cartilage; matrix; osteoarthritis; repair; vascularisation; mineralisation; differentiation; ss.
   Score 22; DB 19; Length 1751;
Pred. No. 0.52;
0; Mismatches 0; Indels (
   Sequence 1751 BP; 394 A; 510 C; 490 G; 357 T; 0 other;
   Pang RHL;
  Sequence encoding osteogenic protein CBMP2B.
  Ozkaynak E,
   Location/Qualiflers
   AAQ53144 standard; cDNA; 1788 BP
  /*tag= a .
/product= CBMP2B
   6.2%; s
100.0%;
  Oppermann H,
   890S-0422699.
90US-0483913.
90US-0569920.
   88US-0179406
   90US-0599543.
  89US-0422613
   90US-0579865
  90US-0621849
  91US-0660162
   92US-0841646
   90US-0600024
   06-JUN-1994 (first entry)
  22; Conservative
  ..1626
   Query Match
Best Local Similarity
  WPI; 1993-395405/49.
   Kuberasampath T,
  P-PSDB; AAR44748
  Homo sapiens.
   07-SEP-1990;
18-OCT-1990;
18-OCT-1990;
  04-DEC-1990;
04-DEC-1990;
22-FEB-1991;
   08-APR-1988;
  US5266683-A
   15-AUG-1988;
23-FEB-1989;
   17-OCT-1989;
17-OCT-1989;
  22-FEB-1990;
20-AUG-1990;
   30-NOV-1993
  08-APR-1988
   20-DEC-1991
  21-FEB-1992
   AAQ53144;
  Rueger DC
  Matches
  AAQ53144
*5555555555555
   ò
  q
```

```
Gaps
   The osteogenic protein when in association with a matrix can induce at the locus of an implant the full development cascade of endochodraal bone formation including vascularisation, mineralisation and bone marrow differentiation. The osteogenic protein can also be used to repair both bone and cartilage in the treatment of osteoarthritis.
  Prepro human CBMP2B; cartilage and endochondrial bone formation; allograft repair; osteoarthritis; non-union fracture repair; osteogenesis; periodontal, dental and craniofacial reconstruction;
   ó
New pure mammalian osteogenic proteins - induce cartilage and endochondral bone formation when in association with a matrix
  6.2%; Score 22; DB 14; Length 1788;
100.0%; Pred. No. 0.52;
ive 0; Mismatches 0; Indels (
  0.52;
has 0; Indels
  Sequence 1788 BP; 418 A; 515 C; 494 G; 361 T; 0 other;
   Pang RHL;
   Kuberasampath T, Oppermann H, Ozkaynak E,
                                Claim 37; Columns 93-96; 128pp; English.
  Location/Qualifiers
403..1629
  AAQ72710 standard; cDNA; 1788 BP
   15 ggaggagggagggagggaagga 36
  8805-0232630

8905-0315342.

8905-0422613.

8905-0422699.

9005-0569920.

9005-0569920.
   90US-0621849.
90US-0621988.
  88US-0179406
  88US-0179406
   90US-0660162.
90US-0810560.
  90US-0600024
  90US-0993387
   (first entry)
  Query Match
Best Local Similarity 100.0
  Prepro human CBMP2B cDNA.
   /*tag=
   (STYC ) STRYKER CORP.
   09-JUN-1995
   Homo sapiens
  17-OCT-1989;
22-FEB-1990;
20-AUG-1990;
07-SEP-1990;
18-OCT-1990;
18-OCT-1990;
   08-APR-1988;
   US5354557-A.
  11-0CT-1994
  04 - DEC - 1990;
04 - DEC - 1990;
  18-DEC-1992;
  08-APR-1988
   23-FEB-1989
   17-0CT-1989
  20-DEC-1991;
   28-JAN-1992;
   21-FEB-1992
   AAQ72710;
  Rueger DC;
  36
  RESULT
  q
  ó
```

us-09-846-456-2.oli.rng

```
AAV15207;
  Query Match
  RESULT 38
AAV15207
δλ
  g
  ö
   Human, osteogenic protein; hOP-1; murine; mOP-1; TGF-beta superfamily; transforming growth factor-beta; dimer; antibody; epitope; hippocampus; purification; implantable osteogenic device; bone formation; cranofacial; anomaly; skeletal; endochrondral bone formation; oraclassin non-union fracture; cartilage repair; osteoarthritis; ss.
   Gaps
  AAQ72710 encodes AAR51654 prepro human CBMP2B, fragments of the related protein CBMP3 (AAR51642) consisting of residues 93-109 and 77-83 are uniglycosylated osteogenic polyeptides. These polypeptides can be disulphide bonded to form a dimer, which forms an essential in a biodegradable matrix which can be implanted into a mammalian bone marrow cavity, here it can induce local cartilage, bone and endochondrial bone formation; and it can also accelerate allograft repair. This implant has the advantage of inducing all stages of bone formation and of having a higher specific activity than other known biosynthetic materials. The implant can be used to repair non-union fractures and cartilage; treat osteoarthritis; and aid
  ;
0
   Implantable device for inducing osteogenesis - comprises porous matrix contg. non-glycosylated dimeric, disulphide linked
   6.2%; Score 22; DB 15; Length 1788; 100.0%; Pred. No. 0.52; tive 0; Mismatches 0; Indels
   in periodontal, dental or craniofacial reconstruction.
  Sequence 1788 BP; 418 A; 515 C; 494 G; 361 T; 0 other;
   Disclosure; Columns 91-96; 128pp; English.
   /*tag= a
/product= Prepro-CBMP2B
   Location/Qualifiers
   AAT02601 standard; cDNA; 1788 BP
   326 ggaggaggagggagggaagga 347
   15 ggaggagggagggaggga 36
  890S-0315342.
890S-0422613.
890S-0422699.
900S-0483913.
   88US-0179406.
88US-0232630.
   92US-0841646
   88US-0179406
  (first entry)
   403..1629
  Query Match 6.2
Best Local Similarity 100.
Matches 22; Conservative
   Human CBMP2(b) cDNA.
         WPI; 1994-324521/40.
  osteogenic protein.
                    P-PSDB; AAR51654
   Homo sapiens
  17-OCT-1989;
22-FEB-1990;
20-AUG-1990;
   08-APR-1988;
   20-JUN-1996
   US5468845-A.
   08-APR-1988
15-AUG-1988
   3-FEB-1989
   2,1-NOV-1995
   21-FEB-1992
  17-0CT-1989
   AAT02601;
   RESULT 37
   AAT02601
   ò
   g
```

```
The sequences given in Anious Line number of CBMP3. These proteins, CBMP2B, CBMP2A and the partial sequence of CBMP3. These proteins have true osteogenic activity when properly folded and dimerised. CBMP2B and CBMP2A may form a heterodimer with mature hop-1. These proteins contain a conserved six or seven cysteine skeleton in their active regions. Probes based on this region have been used in the solution of further osteogenic protein family members. Fragments of these proteins can be used in the production of dimeric peptides which may be used in the generation of antibodies with binding specificities for osteogenic proteins. The antibodies with binding specificities for osteogenic proteins. The antibodies with binding specificities of proteins of the osteogenic protein and may be used in purification protocols. Osteogenic proteins, such as these, may be used in an implantable osteogenic device which allows predictable bone in an implantable osteogenic device which allows predictable bone formation correct acquired and congenital cranôferial and other skeletal or dental anomalies. They may be used to induce local endochrondral bone formation in non-union fractures and in other clinical applications including dental and periodontal applications including dental and periodontal applications including central and periodontal applications including central and periodontal applications where bone formation is required. Other potential applications include cartilage repair, e.g. in the treatment of osteoarthritis. This sequence was repair, e.g. in the breatment of osteoarthrities.
  Gaps
   Antibodies with osteogenic protein binding specificity - used in purification of osteogenic proteins, and as antigenic proteins
  Human; osteogenic protein; subunit; endochondral bone formation;
  The sequences given in AAT02601-03 encodes the human osteogenic
  ;
0
   6.2%; Score 22; DB 17; Length 1788;
  Indels
  Ozkaynak E, Rueger DC;
   Sequence 1788 BP; 418 A; 515 C; 494 G; 361 T; 0 other;
   COITE 12,
Pred. No. 0.52;
  Human osteogenic protein CBMP2B encoding cDNA.
  Mismatches
   Disclosure; Column 93-96; 129pp; English
   Location/Qualifiers 403..1629
   AAV15207 standard; cDNA; 1788 BP
  dimeric; recombinant protein; ss.
   Ouery Matcn
Best Local Similarity 100.0%; Pi
مرماه کیستوسید
  326 ggaggaggaggaaggaagga 347
  Kuberasampath T, Oppermann H,
  15 ggaggagggagggagggaagga 36
900S-059543
900S-0616374
900S-0621849
900S-0621988
910S-0660162
910S-0810560
920S-0827052
  93US-0147023
  27-MAY-1998 (first entry)
   /*tag= a
  (STYC ) STRYKER CORP.
  WPI; 1996-010159/01.
   P-PSDB; AAR85761.
   Homo sapiens.
   04-DEC-1990;
04-DEC-1990;
   22-FEB-1991;
   20-DEC-1991;
28-JAN-1992;
           18-OCT-1990;
   21-NOV-1990;
  01-NOV-1993;
```

(first entry)

16-DEC-1999

AAZ27580;

```
The present sequence encodes a human osteogenic protein, which is used in the present invention. The present invention describes methods for selectively extracting an osteogenic protein (OP) from a mixture. The method comprises: (a) exposing the mixture to an antibody that specifically binds OP, separating the resulting antibody-protein complex from the mixture, and dissociating the complex. In the methods OP comprises a pair of oxidised subunits that are disulphide-bonded to form a dimer, and one of the subunits has an amino acid (aa) sequence designated OPS, sequence given in the specification. In dimeric form OP is capable of inducing cartilage and endochondral bone formation in a mammal when disposed within a matrix implanted in the mammal. The
   Extraction of osteogenic protein from mixture - using antibodies specific for novel polypeptide chains useful as subunit(s) of dimeric osteogenic protein(s)
   Kuberasampath T, Oppermann H, Ozkaynak E, Pang RHL;
   Sequence 1788 BP; 418 A; 515 C; 494 G; 361 T; 0 other;
/function= "Osteogenic protein"
/product= "CBMP2B"
   Disclosure; Column 89-94; 127pp; English.
   95US-0447570
   88US-0232630.
89US-0315342.
   90US-0599543
   89US-0422699
  90US-0483913
90US-0569920
  90US-0579865
   90US-0621988
  91US-0660162
   91US-0810560
92US-0827052
  90US-0616374
  90US-0621849
   95US-0447570
  (STYC ) STRYKER CORP.
   WPI; 1998-158353/14.
  93US-
  P-PSDB; AAW44304
  18-OCT-1990;
18-OCT-1990;
21-NOV-1990;
   17-OCT-1989;
17-OCT-1989;
22-FEB-1990;
   23-MAY-1995;
                                      US5714589-A
   07-SEP-1990;
  20-AUG-1990;
   04-DEC-1990;
  04-DEC-1990;
  03-FEB-1998
   15-AUG-1988
  01-NOV-1993
   23-MAY-1995
   Rueger DC,
   23-FEB-1
  22-FEB-1
   20-DEC-
   28-JAN-
```

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ö
                               Gaps
                               ;
6.2%; Score 22; DB 19; Length 1788; 200.0%; Pred. No. 0.52;
              100.0%;
                           22; Conservative
              Best Local Similarity
 Query Match
```

```
0; Indels
0; Mismatches
               326 ggaggaggagggaggaagga 347
                         Matches
                            д
                õ
```

ö

Gaps

ö

0; Indels

Mismatches

6.20, 100.0%; Pre

22; Conservative

Matches

Best Local Similarity

Query Match

326 ggaggagggagggagga 347 

ŏ q

Score 22; DB 20; Length 1788; Pred. No. 0.52;

Sequence 1788 BP; 418 A; 515 C; 494 G; 361 T; 0 other;

```
AAZ27580 standard; cDNA; 1788 BP
RESULT 39
            AAZ27580
ID AAZ2
```

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The invention relates to a device for implantation in a mammal comprising a chondrogenic protein (1) dispersed within a biocompatible, in vivo degradable matrix defining pores which permits the influx, prolliferation and differentiation of migratory progenitor cells, where (1) comprises a substantially pure protein with the amino acid sequence VPKPCCAPT, which is capable of inducing cartilage formation. The device is used as an allogenic or xenogenic implant for the induction endochondral bone formation in mammals.
  Chondrogenic protein; biodegradable matrix; cell proliferation; cell differentiation; migratory progenitor cell; cartilage formation; allogenic implant; xenogenic implant; endochondral bone formation; osteogenic protein; CBMP2; ss.
  Rueger DC, Pang RHL, Kuberasampath T, Ozkaynak E, Oppermann H;
  This sequence encodes the human CBMP2B protein.
  Disclosure; Column 89-93; 127pp; English.
  Human prepro CBMP2B coding sequence.
   88US-0179406.
88US-0232630.
92US-0841646.
89US-0422699.
90US-0621988.
  (STYC ) STRYKER BIOTECH CORP
  93US-0147023.
89US-0315342.
  90US-0569920
90US-0579865
   910S-0660162
   90US-0599543
   90US-0616374
   91US-0810560
   89US-0422613
   90US-0483913
   90US-0621849
  WPI; 1999-589530/50.
   P-PSDB; AAY43112.
   Homo sapiens
  17-OCT-1989;
04-DEC-1990;
22-FEB-1991;
  01-NOV-1993;
23-FEB-1989;
17-OCT-1989;
  22-FEB-1990;
20-AUG-1990;
07-SEP-1990;
  24-MAY-1995;
   08-APR-1988;
15-AUG-1988;
21-FEB-1992;
   US5958441-A.
   28-SEP-1999
   18-OCT-1990;
   18-0CT-1990
   21-NOV-1990
   04-DEC-1990
   20-DEC-1991
```

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RESULT

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The present invention describes isolated DNA (I) encoding at least one osteogenically active region of human osteogenic protein-1 in prepro form (OP1-PP), murine OP2-PP or human OP2-PP. Also described are: (A) DNA related to (I) encoding a polypeptide able to form dimers that can induce cartilage and endochondral bone formation in a mammal when implanted in a matrix; (B) vectors containing (I) or related DNA; (C) host cells transformed with this vector; (D) DNA (I') encoding a prepro- or pro-OP1, and related vectors and transformed
  Nucleic acid encoding mammalian osteogenic proteins in prepro form - able to induce cartilage and bone formation when implanted in matrix, useful for repairing bone defects
  Human; osteogenic protein; OP-1; OPX; endochondral bone formation; cartilage; craniofacial defect; skeletal disorder; dental disorder; non-union fracture; osteoarthritis; vascularisation; mineralisation; bone marrow differentiation; ss.
   Kuberasampath T, Oppermann H, Ozkaynak E, Pang RHL;
   "osteogenic protein"
  Human osteogenic protein CBMP2B encoding cDNA.
  Disclosure; Column 89-92; 127pp; English.
   Location/Qualifiers
   /product= "CBMP2B
          AAX00232 standard; cDNA; 1788 BP
  91US-0660162.
91US-0810560.
92US-0827052.
  90US-0616374.
   95US-0449700
   32US-0841646
   88US-0179406.
88US-0232630.
   89US-0422613
   89US-0422699
   90US-0483913
  90US-0569920
  90US-0599543
  900S-0600024
   90US-0621849
  90US-0621988
   95US-0449700
  93US-0147023
   /function=
   (first entry)
   403..1629
   /*tag=
  (STYC-) STRYKER CORP.
   WPI; 1999-131303/11.
  P-PSDB; AAW89681.
  sapiens
  23-MAY-1995;
   22-FEB-1990;
20-AUG-1990;
  18-0CT-1990;
18-0CT-1990;
  24-MAR-1999
   US5863758-A.
   23-FEB-1989;
  -OCT-1989;
  17-0CT-1989;
  21-NOV-1990;
   04-DEC-1990;
   28-JAN-1992
01-NOV-1993
   23-MAY-1995
   26-JAN-1999
   5-AUG-1988
  04-DEC-1990
   22-FEB-1991
   20-DEC-199
   Rueger DC
                                   AAX00232;
   07-SEP-1
  Homo
AAX00232
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  polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
mammalian cells, able to induce bone and cartilage formation; (F) mature opt secreted from mammalian cells following expression of the sequence that encodes horl-PP; and (G) production of an active osteogenic composition by truncating mature opt protein. Host cells of (C) are used to produce proteins able to induce cartilage and bone formation, e.g. for correction of acquired or congenital craniofacial defects or other skeletal or dental disorders; to heal non-union fractures; to repair cartilage, e.g. in osteoarthritis, or generally wherever bone formation is required. The proteins induce complete development of endochondral bone, including vascularisation, mineralisation and bone marrow differentiation. The present sequence encodes human CBMP2B.
   Gaps
  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
   ;
0
  6.2%; Score 22; DB 20; Length 1788;
100.0%; Pred. No. 0.52;
   The invention relates to isolated polynucleotide (I) and
   0; Indels
   Sequence 1788 BP; 418 A; 515 C; 494 G; 361 T; 0 other;
   DNA encoding novel human diagnostic protein #15183.
   0; Mismatches
  Claim 1; SEQ ID No 15183; 103pp; English.
  AAS79379 standard; cDNA; 1832 BP
  326 ggaggagggagggaggga 347
   15 ggaggagggagggagggagga 36
  Tang YT;
  100.08;
  31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
   30-MAR-2001; 2001WO-US08631.
  13-FEB-2002 (first entry)
   Conservative
  Drmanac RT, Liu C,
   WPI; 2001-639362/73
   Best_Local Similarity
Matches 22; Conserv
   (HYSE-) HYSEQ INC
  P-PSDB; ABG15192
  WO200175067-A2.
   Homo sapiens.
  biodiversity
   11-0CT-2001
  AAS79379;
  Query Match
   AAS79379/c
  a
  δλ
                 $$$$$$$$$$$$$$$$$$$
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.;
0
imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and annino acid sequences. AAS64197-AAS94564 represent novel human Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the WIPO.int/pub/published_pct_sequences.
  Gaps
   bone morphogenic protein; BMP 2B; cartilage; periodontal disease;
tissue repair; osteoporosis; treatment; oligonucleotide probe; ss.
  /note= "BMP-2B contains at least this part of the
   ;
  DB 23; Length 1832; 0.52;
   0; Indels
  Sequence 1832 BP; 447 A; 439 C; 432 G; 484 T; 30 other;
   /*tag= b
/product= Bone-morphogenic_protein_2B
1333..1626
   6.2%; Sco...
100.0%; Pred. No. v...
"... 0; Mismatches
  Human bone morphogenic protein (BMP) 2B cDNA.
   Location/Qualifiers
   sednence,
   1321 AGGAGGGAGGGAGGAAG 1300
   AAT78942 standard; cDNA; 1944 BP.
   328 аддадддадддадддааддаад 349
  Rosen VA, Wang EA, Wozney JM;
  86US-0943332.
87US-0028285.
88US-0179100.
  93US-0118363
  89US-0378537
  92US-0884353
   93US-0118363
  86US-0880776
  1630..1938
   22-JAN-1998 (first entry)
   /*tag= a
403..1629
   22; Conservative
  (GEMY ) GENETICS INST INC
  /*tag=
   8..402
   Local Similarity
   WPI; 1997-288573/26.
P-PSDB; AAW24850.
  Homo sapiens
   18-MAY-1992;
07-SEP-1993;
01-JUL-1986;
  07-SEP-1993;
   US5631142-A.
   mat_peptide
   20-MAY-1997
   11-JUL-1989
  17-DEC-1986
  08-APR-1988
   20-MAR-1987
   AAT78942;
   Query Match
   Key
5'UTR
   RESULT 42
   Matches
  3'UTR
   CDS
  AAT78942
  Best
   ò
    555555555555
```

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The HindIII-SacI bovine genomic bBMP-2 fragment described in AAN80627 is subcloned into M13, labelled and used as probe to screen bolyadenylated RNAs from various cells and tissue sources. Sequence analysis of the weakly hybridising recombinants hBMP-2 class II (=BMP-4) indicated that they are quite homologous with the sequence given in AAN80622 at the end of their coding regions, but less so in
   This cDNA sequence encodes the human bone morphogenic protein (BMP) 2B. Oligonucleotide probes were synthesised based on a partially sequenced BMP-2B protein isolated from ground bowine powder. The probes were used to screen a bowine liver DNA library to obtain the BMP-2B encoding DNA sequence. The DNA was used to screen a U-2 OS human cell line cDNA library to obtain this human BMP-2B cDNA. BMPs can be used to induce bone and cartilage formation, and in wound healing and tissue repair. They can also be used for treating periodontal disease or osteoporosis.
  Bone morphogenic protein; hBMP-2 class II; probes; cartilage formation; bone formation; osteogenic cpds; prodontal disease; ss.
  Gaps
Production of human bone morphogenic protein 2A or 2B in cell culture - useful inducing bone or cartilage production, in wound healing and tissue repair
   Bone morphogenic proteins - obtd. using recombinant DNA and used for inducing cartilage and bone formation.
  ö
   6.2%; Score 22; DB 18; Length 1944;
100.0%; Pred. No. 0.52;
tive 0; Mismatches 0; Indels 0
   Human Bone Morphogenic Protein-2 class II cDNA from U2OS-3.
  Sequence 1944 BP; 488 A; 535 C; 510 G; 411 T; 0 other;
  /product=hBMP-2 class II
  Location/Qualifiers
  Example 5; Fig 3; 22pp; English.
   AAN80634 standard; DNA; 1954 BP.
  326 ggaggagggagggagga 347
   15 ggaggaggagggagggaagga 36
  87US-0031346.
   87WO-US01537
   Disclosure; ; 7pp; English.
  08-OCT-1990 (first entry)
  (GENE-) GENETICS INST INC.
  22; Conservative
   ..1623
   Wozney JM, Rosen VA;
  Similarity
  WPI; 1988-021565/03.
  P-PSDB; AAP80620
  Homo sapiens
  26-MAR-1987;
   WO8800205-A
  14-JAN-1988.
   Query Match
Best Local S
   AAN80634;
  Matches
   AAN80634
  RESULT
   δ
   g
```

bone fractures; improved fixation of artificial joints; in cosmetic plastic surgery; and in treatment of periodontal disease, burns,

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  The sequence was obtd. from clone lambda U2OS-3 (ATCC 40342) which was isolated from a cDNA library prepd. using human cell line U-2 OS RNA. It is one of two classes of clones isolated distinguished by hybridisation characteristics. This class, designated hBMP-2B (previously BMP-4 and BMP-2 Class II) hybridised only weakly with the probe which was derived from the bovine BMP-2A sequence, and showed only partial homology with that sequence. The second class, hBMP-2A (previously BMP-2 and BMP-2 class I) hybridised strongly and was much more homologous. The gene prod. is an oseteoinductive protein useful for inducing bone/cartilage repair, wound healing and tissue repair. Typical applications include healing of
      Human cDNA hBMP-2 class II contains an opem reading frame of 1224 bp, encoding a protein of 408 amino acids. The protein is preceded by a 5' untranslated region of 394 bp with stop codons in all frames, and contains a 3' untranslate dregion of 308 bp following the in-frame stop codon. The 8 bp region preceding this 5' untranslated region represents a linker used in the cDNA cloning procedures. See also AAN80619-N80636 and AAN81963-64.
  Gaps
  New DNA sequences encoding osteo-inductive protein - useful for stimulating bone and cartilage re formation e.g. for wound healing and tissue repair.
   .;
0
  6.2%; Score 22; DB 9; Length 1954; 100.0%; Pred. No. 0.52; ive 0; Mismatches 0; Indels
   Sequence 1954 BP; 492 A; 536 C; 511 G; 415 T; 0 other;
  Bone; cartilage; osteoinductive protein; ss.
  Location/Qualifiers
  /*tag= b
/label= claim 1(c)
  Disclosure; Fig 3; 20pp; English.
  326 ggaggaggagggagggaagga 347
  AAQ14037 standard; DNA; 1954 BP
   15 ggaggagggagggagggagga 36
  Human BMP-2B in lambda U20S-3.
  88US-0179100.
   86US-0880776
  88US-0179100
   (first entry)
   (GENE-) GENETICS INST INC.
   402.1626
   403..1629
  22; Conservative
   /*tag=
   WPI; 1991-309401/42.
P-PSDB; AAR14242.
   Best Local Similarity
the more 5' regions
  Homo sapiens
   01-JUL-1986;
   04-APR-1988;
   08-APR-1988;
   13-JAN-1992
   US5013649-A.
  07-MAY-1991
   Query Match
  AAQ14037
   Misc_RNA
   44
  Matches
   CDS
   AAQ14037
   δλ
   g
8.5555555555
```

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A human U20S CDNA library was screened with a bovine BMP-2A probe (see AAQ31868). Sequence analysis of strongly hybridising clones designated hBMP-2A (previously designated BMP-2 and BMP-2 Class I) indicated that they have extensive homology with the partial bovine BMP-2A sequence; weakly hybridising clones were designated hBMP-2B (previously designated BMP-4 and BMP-2 Class II) and sequence
   Gaps
  Bone Morphogenic Protein; bacteriophage lambda U2OS-3; ATCC 40342; bone fracture; cartilage defect; osteoporosis; ss.
   DNA encoding osteo-inductive proteins - used for producing BMP-2A and BMP-2B for inducing bone or cartilage formation and wound
   /*tag= b
/note= "nucleotides 1-8 are from cloning vector"
1627..1954
  ;
  DB 12; Length 1954; 0.52;
   0; Indels
                   incisions, ulcers etc.
See also AAQ14035 and AAQ14036, AAQ14909 and AAQ14910.
  Seguence 1954 BP; 493 A; 536 C; 511 G; 414 T; 0 other;
   6.2%; Score 22; DB 100.0%; Pred. No. 0.5 tive 0; Mismatches
  /*tag= a
/product= pre-pro-BMP-2B
  Location/Qualifiers
   AAQ31870 standard; DNA; 1954 BP
  Rosen VA, Wang EA, Wozney JM;
  Claim 2; Fig 3; 22pp; English.
  15 ggaggagggagggagga 36
  86US-0943332.
87US-0028285.
88US-0179100.
  89US-0378537
   86US-0880776
  89US-0378537
  16-APR-1993 (first entry)
   (GEMY ) GENETICS INST INC
  /*tag= c
  Query Match
Best Local Similarity 100.C
Matches 22; Conservative
   ..1629
   Human BMP-2B sequence.
  WPI; 1992-414955/50.
  P-PSDB; AAR29282
  17-DEC-1986;
20-MAR-1987;
08-APR-1988;
  Homo sapiens
  11-JUL-1989;
  US5166058-A.
  01-JUL-1986;
  11-JUL-1989;
  24-NOV-1992
   AAQ31870;
  healing
   3'UTR
  45
  5'UTR
  AAQ31870
  RESULT
  á
  ద
22222×3
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analysis indicated these clones were quite homologous with the bounders sequence at their 3' end but less so at the 5' end. A clone where sequence at their 3' end but less so at the 5' end. A clone when the constant and the second and the second and the clone state of the BMP-2B recombinant II-10-1, then secondary hybridisation of consitive clones to a 31mer probe (AAQ37828 - also derived from II-10-1). The clone U2OS-3 was isolated and its insert sequenced. This clone consisted as ATCC 40342.
```

SQ Sequence 1954 BP; 492 A; 536 C; 511 G; 415 T; 0 other;

Query Match
6.2%; Score 22; DB 13; Length 1954;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 326 ggaggagggagggaggaagga 347
Db 15 ggaggagggagggaagga 36

Search completed: September 20, 2002, 06:07:38 Job time: 10342 sec

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September 20, 2002, 06:14:47; Search time 111.56 Seconds (without alignments) 786.045 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
   Total number of hits satisfying chosen parameters:
  383533 seqs, 122816752 residues
   Post-processing: Listing first 45 summaries
  OM nucleic - nucleic search, using sw model
  OLIGO_NUC
Gapop 60.0 , Gapext 60.0
  Minimum DB seq length: 0
Maximum DB seq length: 200000000
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357
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  Scoring table:
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  Run on:
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Issued\_Patents\_NA:\* Database :

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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description           | Sequence 1, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 7, Appli<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 5, Appli<br>Sequence 5, Appli<br>Sequence 5, Appli<br>Sequence 5, Appli<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 16, Appli<br>Sequence 16, Appli<br>Sequence 16, Appli<br>Sequence 16, Appli<br>Sequence 17, Appli<br>Sequence 16, Appli<br>Sequence 17, Appli<br>Sequence 27, Appli<br>Sequence 27, Appli<br>Sequence 27, Appli<br>Sequence 22, Appli<br>Sequence 22, Appli                                                                                                                                                                                                   |
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| SUMMARIES             | US-09-308-406-1<br>US-09-308-406-1<br>US-07-841-646-6<br>US-07-901-703-18<br>US-08-447-023-6<br>US-08-449-700-6<br>US-08-449-700-6<br>US-08-449-700-6<br>US-08-449-699A-6<br>PCT-US33-05446-18<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3<br>US-08-90-11-3 |
| DB                    | 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| Length                | 1456<br>1788<br>1788<br>1788<br>1788<br>1788<br>1788<br>1954<br>1954<br>1954<br>1954<br>1954<br>1954<br>1954<br>1954                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| %<br>Query<br>Match I |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| Score                 | 100001110000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| Result<br>No.         | C C C C C C C C C C C C C C C C C C C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |

| 28 19 5.3 654 2 05.08-975-316-9 Sequence 9, Appl 20 19 5.3 664 2 05.08-975-316-9 Sequence 9, Appl 30 19 5.3 664 2 05.08-075-717-8 Sequence 1, Appl 31 18 5.0 2407 4 05.08-707-88 Sequence 1, Appl 34 18 5.0 2407 4 05.08-707-88 Sequence 1, Appl 35 18 5.0 2407 9 Sequence 1, Appl 35 18 5.0 6386 2 05.08-707-31-1 Sequence 1, Appl 36 18 5.0 6386 2 05.08-707-31-1 Sequence 1, Appl 36 19 5.0 6386 2 05.08-707-31-1 Sequence 1, Appl 36 19 10 10 10 10 10 10 10 10 10 10 10 10 10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     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| 19 5.3<br>19 5.3<br>19 5.3<br>19 5.3<br>18 5.0<br>28 5.0<br>28 5.0<br>29 2.2<br>18 5.0<br>20 2<br>21 8 5.0<br>20 6<br>17 4.8<br>17 6.15696<br>19 6.15696<br>10 6.15696<br>10 6.15696<br>10 7 4.8<br>11 7 4.8<br>11 1 4.8<br>12 10 10 NOENTION: March CAPICATION: March CAPICATION: March CAPICATION NOENTION: March CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAPICATION: CAP | 040m40m40m00m04444                                           | ALIGNMENTS  1 US/09308406  2 in  1 US/09308406  2 in  2 in  3 in  3 in  3 in  4 in  5 in  5 in  6 in  6 in  6 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  7 in  | 22; 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PPLICANT: Van den Wi TTLE OF INVENTION: WA TTLE OF INVENTION: WA TTLE OF INVENTION: WA TTLE REFERENCE: 1/962 TIER REFERENCE: 1/962 TIER REFERENCE: 1/962 TRENT APPLICATION N URRENT FILING DATE: ARLIER PILING DATE: ARLIER FILING DATE: CONTWARE: PALCATION N ARLIER FILING DATE: CONTWARE: PALCATION N TUMBER OF SEQ ID NOS: UND HO 1 LENGTH: 1456 TYPE: DNA ORGANISM: human                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Local Similarity Local Similarity Local Sinilarity Local Siz; Conserv 22; Conserv 187 ggaggaggaggaggaggaggaggaggaggaggaggagga                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| 28 29 29 30 31 31 31 32 33 34 34 35 34 35 34 35 37 38 38 38 38 38 38 38 38 38 38 38 38 38                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              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FILING DATE: 23-JAN-1995
CLASSIFICATION: 514
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APPLICATION NUMBER: US/07/841,646
FILING DATE: 19920221
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   OSTEOGENIC DEVICES
   APPLICANT: OPPERMANN, HERNANN
APPLICANT: OPRERASANDATH, THANGAVEL
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TILLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/243,435
FILING DATE:
APPLICATION NUMBER: US/08/117,367
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
  NAME: Corstanje, Brahm J.
REGISTRATION UNDABER: 34,804
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-245-2858
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1751 base pairs
TYPE: nucleic acid
STRANDENNESS: double
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FILING DATE: 28-JAN-1992
   APPLICATION NUMBER: US 810,560 FILING DATE: 20-DEC-1991
   Sequence 6, Application US/07841646
Patent No. 5266683
GENERAL INFORMATION:
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   STATE: MASSACHUSETTS
COUNTRY: U.S.A.
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APPLICATION NUMBER: 05 600,024
FILING DATE: 18-OCT-1990
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FILING DATE: 18-OCT-1990
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FILING DATE: 07-SEP-1990
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FILING DATE: 22-FEB-1990
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FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-ARR-1988
ATTORNEY/AGATION:
                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FITTING DATE: 04-DEC-1990
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
   NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-(TELECOMMUNICATION INFORMATION: TELEPHONE: 617/248-7000
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   INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: TENGTH: 1788 base pairs
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APPLICANT: RUBERSAMPATH, THANGAVEL
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZAKAYNAK, ENGIN
TITLE OF INVENTION: PROSTHERIC DEVICES HAVING ENHANCED
TITLE OF INVENTION: OSTEOGENIC PROPERTIES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/07/901,703

FILING DATE: 19920616

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 27,829

REFERENCE/DOCKET NUMBER: STK-057

TELEPHONE: 617/248-7000

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
  HOMO SAPIENS
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  TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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  BOSTON
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US-08-147-023-6
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Sequence 6, Application US/08147023

BERERAL INFORMATION:

APPLICANT: OFFERNANN HERMANN
APPLICANT: ORGANNAK, ENGIN
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COUNTRY: MASSACUSETTS
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STATE: MASSACUSETTS
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FILING DATE: 20-DEC-1991
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FILING DATE: 21-FEB-1992
CLASSIFICATION: 536
  APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUBGER, DAVID C.
APPLICANT: ROBGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
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   IDENTIFICATION METHOD: experimental
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
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LOCATION: 403..1626
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MOLECULE TYPE: CDNA
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FILING DATE: 18-OCT-1990
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FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTONEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEE-1990
PRIOR APPLICATION DATA:
  FILING DATE: 18-OCT-1990
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APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
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INFORMATION FOR SEQ ID NO: 6:
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ORGANISM: HO
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Patent No. 595841

GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: ANGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
NUMBER OF SEQUENCES:
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FILING DATE: 24 MAY-1995
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FILING DATE: 01-NOV-1993
              APPLICATION NUMBER: US 179,460
FILING DATE: 08-ARR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ 1D NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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  ORGANISM: HOMO SAPIENS
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REFERENCE/DOCKET NUMBER: 3TK-001CP6CN
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/248-7000
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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LENGTH: 1788 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDNUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-057
TELECOMMULTCATION INFORMATION:
TELEPHONE: 617/248-7000
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LENGTH: 1788 base pairs
TYPE: NUCLEIC ACID
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  TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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ADDRESSEB: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
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SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,132A
   APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
  ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1994 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
   NAME/KEY: CDS
LOCATION: 403..1626
IDENTIFICATION METHOD: experimental
  Osteosarcoma Cell Line
U-20S
   ; Sequence 3, Application US/08050132A; Patent No. 5661007
   COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOCOMMON
   15 GGAGGGGGGGGGGGGAAGGA 36
  TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
   ORGANISM: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
  Homo sapiens
STRANDEDNESS: single
   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
   FILING DATE:
CLASSIFICATION: 435
                                   MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ONGINAL SOURCE:
ORGANISM: HOMO SAPI
                      linear
   GENERAL INFORMATION:
   ΩS
  ANTI-SENSE: NO ORIGINAL SOURCE:
   COUNTRY: US
ZIP: 02140
   STATE: MA
   US-08-050-132A-3
  ORGANISM:
   FEATURE:
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Indels

Best Local Similarity 100.0%; Pred. No. 0.053; Matches 22; Conservative 0; Mismatches 0;

δy

```
0;
   Gaps
   APPLICANT: Israel, David
APPLICANT: Wolfman, Nell M.
TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.
CORRESPONDENCE: 30
CORRESPONDENCE ADDRESS:
   ö
   Query Match 6.2%; Score 22; DB 1; Length 1954; Best Local Similarity 100.0%; Pred. No. 0.053; Matches 22; Conservative 0; Mismatches 0; Indels
   ADDRESSEE: Legal Affairs, Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: MA.
  MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,847
   ATTORNEY/AGENT INFORMATION:
NAME: KAPIONS, ELLEN J.
REGISTRATION NUMBER: 3,245
REFERENCE/DOCKET NUMBER: GI-5192B
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEFAX: 617-876-5851
IMMEDIATE SOURCE:
LIBRARY: U20S CDNA in Lambda gtl0
CLONE: Lambda U20S-3
POSITION IN GENOME:
UNITS: bp
   Sequence 3, Application US/07989847
Patent No. 5866364
GENERAL INFORMATION:
  326 ggaggaggaggaggaagga 347
  15 GGAGGAGGGAGGGAGGA 36
  TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1954 base pairs
  MOLECULE TYPE: DNA (genomic)
  NAME/KEY: mat_peptide LOCATION: 1279..1626
  TYPE: nucleic acid
STRANDEDNESS: double
  COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
   ATURE:
NAME/KEY: CDS
TOTATION: 403..1629
   FILING DATE:
CLASSIFICATION: 436
   403..1626
  NAME/KEY: mRNA
LOCATION: 9..1934
  COUNTRY: USA
ZIP: 02140-2387
   ; NAME/KEY:
; LOCATION:
US-07-989-847-3
  US-08-050-132A-3
   JS-07-989-847-3
   FEATURE:
   FEATURE
   RESULT 11
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DB 2; Length 1954;

6.2%; Score 22;

Query Match

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,222A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/254,353
   FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Rapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELERAX: (617) 876-1170
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERICSICS:
LENGTH: 1954 base pairs
  LIBRARY: U2OS CDNA in Lambda gt10
CLONE: Lambda U2OS-3
POSITION IN GENOME:
  ORGANISM: Homo sapiens
CELL TYPE: Osteosarcoma Cell Line
CELL LINE: U-20S
   Sequence 3, Application US/08750222A Patent No. 6034061
TOPOLOGY: linear
MOLECTLE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
  mat_peptide
1279..1626
   TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
  403..1629
  mRNA
9..1934
   IMMEDIATE SOURCE:
   NAME/KEY: CDS
  02140
  NAME/KEY:
LOCATION:
FEATURE:
  LOCATION:
  NAME/KEY:
LOCATION:
   RESULT 12
US-08-750-222A-3
  COUNTRY:
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US-08-750-222A-3

US-08-815-652B-3

0; Gaps

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6.2%; Score 22; DB 3; Length 1954;
100.0%; Pred. No. 0.053;
tive 0; Mismatches 0; Indels
  ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC. STREET: 87 CAMBRIDGEPARK DRIVE
  CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/721,847A

FILING DATE: 14-JUN-1991

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Rapinos, Ellen J.

REGISTATION NUMBER: 31,245

REFERENCE/DOCKET NUMBER: 5160C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-876-1170

TELEPHONE: 617-876-1170

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

TENDOMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
   GENERAL INFORMATION:
APPLICANT: Wang, Vicki A.
APPLICANT: Rosen, Vicki A.
APPLICANT: Wozney, John M.
APPLICANT: Wozney, John M.
TITLE OF INVENTION: No. 6150328el BMP Products
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
   LIBRARY: U2OS CDNA in Lambda gt10
CLONE: Lambda U2OS-3
POSITION IN GENOME:
   ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  ; Sequence 5, Application US/07721847A; Patent No. 6150328
   326 ggaggagggagggaggga 347
  15 GGAGGAGGGAGGGAAGGA 36
  TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
   LENGTH: 1954 base pairs.
TYPE: nucleic acid
STRANDEDNESS: double
   Query Match 6.2%
Best Local Similarity 100.(
Matches 22; Conservative
   ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
IMMEDIATE SOURCE:
  403..1629
   mRNA
9..1934
  CAMBRIDGE
   USA
  LOCATION:
   RESULT 14
US-07-721-847A-5
  NAME/KEY:
  NAME/KEY:
   LOCATION:
FEATURE:
   NAME/KEY:
  ; LOCATION:
US-07-721-847A-5
   COUNTRY:
   οy
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   Gaps
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Query Match 6:2%; Score 22; DB 3; Length 1954; Best Local Similarity 100.0%; Pred. No. 0.053; Matches 22; Conservative 0; Mismatches 0; Indels
   ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,652B
   APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
APPLICANT: Celeste, Anthony
APPLICANT: Thies, R. Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KAPIDOS, ELIEN J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186D
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEPHONE: (617) 876-1170
TELEPHONE: (617) 876-1170
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TELEPHONE: (617) 876-1170
TELEPHONE: (617) 876-1170
TELEPHONE: (617) 876-1170
TELEPHONE:
   ORGANISM: Homo sapiens
CELL TYPE: Osteosarcoma Cell Line
CELL LINE: U-20S
IMMEDIATE SOURCE:
  LIBRARY: U2OS CDNA in Lambda gt10
CLONE: Lambda U2OS-3
POSITION IN GENOME:
UNITS: bp
  Sequence 3, Application US/08815652B Patent No. 6034062 GENERAL INFORMATION:
   326 ggaggaggaggaggaagga 347
   15 GGAGGGGGGGGGGGAGGA 36
  MOLECULE TYPE: CDNA to mRNA
  Floppy disk
   NAME/KEY: mat_peptide LOCATION: 1279..1626
  ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
  NAME/KEY: CDS
LOCATION: 403..1629
  mRNA
9..1934
   linear
  0
N
   ANTI-SENSE: NO
ORIGINAL SOURCE:
   ns
   FILING DATE:
   HYPOTHETICAL:
   ADDRESSEE:
  STATE: MA
  NAME/KEY:
LOCATION:
   RESULT 13
US-08-815-652B-3
  COUNTRY:
  FEATURE
   ò
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NAME/KEY:
  SOFTWARE:
  ANTI-SENSE:
   US-08-925-779-5
   Query Match
   STATE:
   FEATURE:
   FEATURE:
  FEATURE
   Matches
   qq
  δŻ
   ó
   ö
   APPLICANT: Israel, David
Wolfman, Neil M.
TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.
   0; Gaps
   Gaps
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0
   Query Match 6.2%; Score 22; DB 4; Length 1954; Best Local Similarity 100.0%; Pred. No. 0.053; Matches 22; Conservative 0; Mismatches 0; Indels
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
  Length 1954;
   0; Indels
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  ATTORNEY/AGENT INFORMATION:

NAME: Kapinos, Ellen J.

REGISTATION NUMBER: 32,245

REFERENCE/DOCKET NUMBER: GI-5192B-CON

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-498-8622

TELEPHONE: 617-497-5851

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
Ouery Match 6.2%; Score 22; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 22; Conservative 0; Mismatches 0
  APPLICATION NUMBER: US/08/469,411
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
  LOCATION: 403..1626
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
  Sequence 5, Application US/08925779; Patent No. 6245889; GENERAL INFORMATION: APPLICANT: Wang, Elizabeth A. APPLICANT: Rosen, Vicki A. APPLICANT: Wozney, John M.
  LENGTH: 1954 base pairs
   TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
  Sequence 3, Application US/08469411
Patent No. 6190880
  326 ggaggaggaggaggaagga 347
  15 GGAGGAGGGAGGGAAGGA 36
  TYPE: nucleic acid
STRANDEDNESS: double
   COUNTRY: USA ZIP: 02140-2387 COMPUTER READABLE FORM: MEDIUM TYPE: Tape
   NUMBER OF SEQUENCES: 30
  CITY: Cambridge
  NAME/KEY:
  GENERAL INFORMATION:
  US-08-925-779-5
  US-08-469-411-3
   RESULT 15
US-08-469-411-3
   RESULT 16
  δ
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Gaps
   ö
  6.2%; Score 22; DB 4; Length 1954;
100.0%; Pred. No. 0.053;
tive 0; Mismatches 0; Indels
TITLE OF INVENTION: No. 6245889el BMP Products
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL ABORESS:
STREET: 87 CAMBRIDGEPARK DRIVE
CITY: CAMBRIDGE
   Patentin Release #1.0, Version #1.25
   IMMEDIATE SOURCE:
LIBRARY: UZOS CDNA in Lambda gt10
CLONE: Lambda UZOS-3
POSITION IN GENOME:
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,779
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  Sequence 3, Application US/08254353A

Patent No. 6287816

GENERAL INFORMATION:

APPLICANT: Rosen, Vicki A.

APPLICANT: Wozney, John M.

APPLICANT: Celeste, Anthony J.
  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/721,847
   5160C
   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: 5160C
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEPHONE: 617-876-1170
TELEPHONE: 617-876-1815
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
   326 ggaggagggagggaggga 347
  15 GGAGGAGGGAGGGAGGAAGGA 36
   TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
  1954 base pairs
  ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
   22; Conservative
   mat_peptide
1279..1629
  LENGTH: 1954 base pai
TYPE: nucleic acid
STRANDEDNESS: double
   CDS
403..1629
  mRNA
9..1934
  Best Local Similarity
  ò
  USA
  FILING DATE:
  COUNTRY: US
  NAME/KEY:
LOCATION:
  Ψ
   NAME/KEY:
  LOCATION:
   LOCATION:
   RESULT 17
US-08-254-353A-3
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ORIGINAL SOURCE:
ORGANISM: HOMO
  STATE: MA
COUNTRY: U
  TOPOLOGY:
  FEATURE:
   ò
  Gaps
  0;
  6.2%; Score 22; DB 4; Length 1954; 100.0%; Pred. No. 0.053; tive 0; Mismatches 0; Indels
APPLICANT: Song, Jeffrey
APPLICANT: Thies, Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSES: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
  ZIP: 02140
CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/254,353A
  FILING DATE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186B
TELECHMONICATION INFORMATION:
TELECHMONE: (617) 876-1170
TELEFAX: (617) 876-1170
TELEFAX: (617) 876-1170
TELEFAX: (617) 876-1170
TELEFAX: (617) 876-1170
TELEFAX: (617) 876-1170
TELEFAX: (617) 876-1170
TELEFAX: (617) 876-1170
TELEFAX: (617) 876-1170
TELEFAX: (617) 876-1170
TELEFAX: (617) 876-1170
  Gequence 3, Application PC/TUS9205374A
GENERAL INFORMATION:
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
   ORGANISM: Homo sapiens
CELL TYPE: Osteosarcoma Cell Line
CELL LINE: U-20S
  LIBRARY: U2OS cDNA in Lambda gt10
CLONE: Lambda U2OS-3
  326 ggaggaggaggaggaagga 347
  15 GGAGGGAGGGAGGGAAGGA 36
   MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO
   LENGTH: 1954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
  Query Match
Best Local Similarity 100.(
Matches 22; Conservative
  NAME/KEY: mat_peptide LOCATION: 1279..1626
  NAME/KEY: CDS
LOCATION: 403.,1629
   9..1934
  linear
  CLONE: Lambda U2
POSITION IN GENOME:
   NAME/KEY: mRNA
   IMMEDIATE SOURCE:
   a
   ORIGINAL SOURCE
   RESULT 18
PCT-US92-05374A-3
  ;
US-08-254-353A-3
   COUNTRY:
  STATE:
   FEATURE
  δ
   g
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Gaps
   °,
   6.2%; Score 22; DB 5; Length 1954;
100.0%; Pred. No. 0.053;
tive 0; Mismatches 0; Indels
  ZIE: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19920625
CLASSIFICATION:
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
  RESULT 19
PCT-US95-07084-3
Sequence 3. Application PC/TUS9507084
GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Rozney, John M.
TITLE OF INVENTION: BMP-9 COMPOSITIONS
TITLE OF INVENTION: BMP-9 COMPOSITIONS
CORRESPONDENCES ADDRESS:
   IMMEDIATE SOURCE:
LIBRARY: UZOS CDNA in Lambda gt10
CLONE: Lambda UZOS-3
POSITION IN GENOME:
  ORGANISM: Homo sapiens
CELL TYPE: Osteosarcoma Cell Line
CELL LINE: U-20S
   ATTORNEY AGENT INFORMATION:
NAME: Rapinos, Ellen J.
REGISTATION UNBER: 32,245
REFERENCE/COCKET NUMBER: GI 51
RELECOMMUNICATION INFORMATION:
TELEFRAN: (617) 876-1170
TELEFRAN: (617) 876-5851
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1954 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
  326 ggaggaggaggaggaagga 347
  15 GGAGGAGGGAGGGAAGGA 36
   CDNA to mRNA
  Query Match
Best Local Similarity 100.0
Matches 22; Conservative
   NAME/KEY: mat_peptide LOCATION: 1279..1626
  NAME/KEY: CDS
LOCATION: 403..1629
  ; NAME/KEY: mRNA
; LOCATION: 9..1934
PCT-US92-05374A-3
  linear
  MOLECULE TYPE: CD
HYPOTHETICAL: NO
ANTI-SENSE: NO
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Gaps
  .;
0
  ö
   Length 1954;
  Ouery Match 5.9%; Score 21; DB 2; Length 445; Best Local Similarity 100.0%; Pred. No. 0.17; Matches 21; Conservative 0; Mismatches 0; Indels
   6.2%; Score 22; DB 6; Length 195
100.0%; Pred. No. 0.053;
.tive 0; Mismatches 0; Indels
   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUBBR: US/08/332,766A FILING DATE: 01-NOV-1994 CLASSIFICATION: 435
   217211/M94/0434/GB
  APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
CORRESPONDENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN DARBY & CUSHWAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
   STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
  Sequence 16, Application US/08332766A Patent No. 5843647 GENERAL INFORMATION:
  NAME: BIED, DONAID J.
REGISTRATION NUMBER: 25,323
REFRENCE/DOCKET NUMBER: 2172:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELERAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 16:
         APPLICATION NUMBER: 28,285
FILING DATE: 20-MAR-1987
APPLICATION NUMBER: 943,332
FILING DATE: 17-DEC-1986
APPLICATION NUMBER: 880,776
FILING DATE: 01-UUL-1986
;SEQ ID NO:5:
  326 ggaggaggaggagggaagga 347
   329 ggagggagggagggaaggaag 349
   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
  SEQUENCE CHARACTERISTICS:
LENGTH: 445 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  Query Match 6.2%
Best Local Similarity 100.0
Matches 22; Conservative
  US-08-332-766A-16/c
  LENGTH: 1954
  US-08-332-766A-16
   5166058-5
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   δλ
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   Gaps
   ö
   Patent No. 5166058; APPLICANT: WANG, ELIZABETH A.; WOZNEY, JOHN M.; RPSEN, VICKI A.; TITLE OF INVENTION: DNA SEQUENCES ENCODING THE OSTEOINDUCTIVE
   6.2%; Score 22; DB 5; Length 1954; illarity 100.0%; Pred. No. 0.053; Conservative 0; Mismatches 0; Indels
   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07084
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
   GI 5186C-PCT
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/378,537
FILING DATE: 11-JUL-1989
FILING APPLICATION DATA:
APPLICATION NUMBER: 179,100
   CELL TYPE: Osteosarcoma Cell Line CELL LINE: U-20S
  : U2OS cDNA in Lambda gtl0
Lambda U2OS-3
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  CLASSIFICATION:
ATTORREY, AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
   326 ggaggagggagggagggaagga 347
   15 GGAGGAGGGAGGGAGGA 36
   TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
  Homo sapiens
   NAME/KEY: mat_peptide LOCATION: 1279..1626
   NUMBER OF SEQUENCES: 19
  403..1629
   Query Match
Best Local Similarity
Matches 22; Conservat
  POSITION IN GENOME:
   IMMEDIATE SOURCE:
  MOLECULE --
HYPOTHETICAL: N
   ORIGINAL SOURCE:
  FILING DATE:
  02140
  ANTI-SENSE:
  ORGANISM:
   NAME/KEY:
   NAME/KEY:
  LOCATION:
   ; LOCATION:
PCT-US95-07084-3
   COUNTRY:
  RESULT 20
5166058-5
   ; PROTEINS
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0
  Query Match 5.9%; Score 21; DB 2; Length 591; Best Local Similarity 100.0%; Pred. No. 0.17; Matches 21; Conservative 0; Mismatches 0; Indels
  0; Indels
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTONEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
TELECOMMUNICATION INFORMATION:
   GENERAL INFORMATION:
APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN DARBY & CUSHWAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
   APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
UNMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New YOLK AVENUE, N.W.
  RESULT 22
US-08-332-766A-17/c
* Sequence 17, Application US/08332766A
* Patent No. 5843647
   Sequence 42, Application US/08332766A Patent No. 5843647 GENERAL INFORMATION:
   TELEPHONE: (202) 861-3000
TELERX: (202) 822-0944
TELEX: 6714627
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 base pairs
TYPE: nucleic acid
STRANDENNESS: single
340 GGAGGGAGGGAGGGAAG 320
   329 ggaggaggaggaaggaag 349
   503 GGAGGGAGGGAAGGAAG 483
  MOLECULE TYPE: DNA (genomic)
  COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
   STREET: 1100 New CITY: Washington
  D. C.
  CITY: Washin
STATE: D. C.
  US-08-332-766A-17
   US-08-332-766A-42
  TOPOLOGY:
  COUNTRY:
  RESULT 23
g
   à
   g
```

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Gaps
   General invariation:

APPLICANT: Chen, H.

APPLICANT: Freimer, N.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

TITLE OF INVENTION: AND TREATING CHROMOSOME-18P RELATED DISORDERS

FILE REFERENCE: 7883-138

CURRENT APPLICATION NUMBER: 09/236,134

EARLIER APPLICATION NUMBER: 09/236,134

EARLIER PILING DATE: 1999-01-22

EARLIER PILING DATE: 1999-10-28

EARLIER FILING DATE: 1998-10-28

EARLIER FILING DATE: 1998-01-28

EARLIER FILING DATE: 1998-01-28

EARLIER FILING DATE: 1998-01-38

EARLIER FILING DATE: 1998-01-38

SARLIER FILING DATE: 1998-03-16

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FASTSEQ for Windows Version 3.0
  ö
  Query Match 5.6%; Score 20; DB 2; Length 278; Best Local Similarity 100.0%; Pred. No. 0.52; Matches 20; Conservative 0; Mismatches 0; Indels
   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 25,323
REGISTRATION SECORET NUMBER: 25,323
RELEVANCE (202) 861-3000
TELEFANX: (202) 861-3000
TELEFANX: (202) 861-3000
TELEFANX: (202) 861-3000
TELEFANX: (202) 861-3000
TELEX: (204) 822-0944
TELEX: (204) 822-0944
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TELEX: (204) 822-0944
TELEX: (204) 822-0944
TELEX: (204) 822-0944
TELEX: (204) 822-0944
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   CATION: all n positions; OTHER INFORMATION: n=a, c, g, or t US-09-268-992-7
  ; Sequence 7, Application US/09268992; Patent No. 6342351
   328 aggagggagggagggagga 347
  ; MOLECULE TYPE: DNA (genomic)
US-08-332-766A-42
   196 AGGAGGGAGGGAAGGA 215
   ORGANISM: Homo sapiens
   linear
   GENERAL INFORMATION:
   72604
  US-09-268-992-7
  SEQ ID NO 7
  TYPE: DNA
```

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   Gaps
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5.6%; Score 20; DB 4; Length 72604; 100.0%; Pred. No. 0.58; tive 0; Mismatches 0; Indels (
  Length 287;
  COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
CLASSIPECATION 1934
CLASSIPECATION AT 35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY AGENT INFORMATION:
NAME: BIRD, Donald J.
   217211/M94/0434/GB
  5.3%; Score 19; DB 2;
   APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
UNMER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
   Sequence 22, Application US/08332766A
Patent No. 5843647
GENERAL INFORMATION:
APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
  Pred. No. 1.7
Mismatches
   STREET: 1100 New York Avenue, N.W.
   Sequence 27, Application US/08332766A Patent No. 5843647
   REFERENCE/DOCKET NUMBER: 2172
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELERAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 base pairs
  100.0%; Pr
   Db 14772 tttcccctcctgctttatct 14791
  NAME: BIRD, Donald J. REGISTRATION NUMBER: 25,323
  MOLECULE TYPE: DNA (genomic) US-08-332-766A-27
  152 GGAGGGAGGGAGGA 170
  75 tttcccctcctgctttatct 94
  329 ggagggagggaggaagga 347
   COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                    Best Local Similarity 100. Matches 20; Conservative
   NUMBER OF SEQUENCES: 125
   Conservative
   TYPE: nucleic acid
STRANDEDNESS: single
  Best Local Similarity
Matches 19; Conserva
  Washington
  linear
  GENERAL INFORMATION:
  RESULT 25
US-08-332-766A-27
  US-08-332-766A-22
  TOPOLOGY:
  Query Match
    Query Match
  RESULT 26
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5.3%; Score 19; DB 2; Length 494;
100.0%; Pred. No. 1.7;
Live 0; Mismatches 0; Indels
  Sequence 9, Application US/08713000
Sequence 9, Application US/08713000
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
APPLICANT: Grieson, Alastair
TITLE OF INVENTION: MATERIALS AND METHODS FOR THE
TITLE OF INVENTION: MADERIALS AND METHODS FOR THE
TURBESPONDENCE 3.15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Speckman Ploard PLLC
   COUNTRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,000
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTORNEY AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REEDENCE/DOCKET NUMBER: 217211/M94/0434/GB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                     CUSHMAN DARBY & CUSHMAN, L.L.P.
   E: Speckman Picard PLLC
2601 Elliott Avenue, Suite 4185
   APPLICATION NUMBER: US/08/332,766A FILING DATE: 01-NOV-1994
  1100 New York Avenue, N.W.
  TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELERX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 22:
  TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-332-766A-22
   331 agggagggagggaaggaag 349
   205 AGGGAGGGAGGAAGGAAG 223
   LENGTH: 494 base pairs TYPE: nucleic acid
   SEQUENCE CHARACTERISTICS:
  Conservative
   single
CORRESPONDENCE ADDRESS:
  FILING DATE:
CLASSIFICATION: 435
  Best Local Similarity
Matches 19; Conserva
   Washington
   STREET: 2601 E CITY: Seattle
  USA
  STRANDEDNESS:
  98121
   RESULT 27
US-08-713-000-9
  COUNTRY:
  CITY: V
STATE:
  STREET:
  Query Match
  STATE:
  g
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0; Indels
   0; Indels
   SOFTWARE: FASTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
FILLING DATE:
   Law Offices of Ann W. Speckman
         Mismatches
   Mismatches
   ADDRESSEE: Law Offices of Ann w. speckmark
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
  NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
  Pred. No.
  Score 19;
  FILING DATE: September 11, 1996 ATTORNEY/AGENT INFORMATION:
   5.3%; Scor.
100.0%; Pre
0;
  CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
       ;
0
  169 gctgggcgtgctggctgag 187
  261 gctgggcgtgctggctgag 279
   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
     19; Conservative
   Conservative
   Diskette
  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
  ; ORGANISM: Pinus radiata
US-09-211-710-9
   Query Match
Best Local Similarity
Matches 19; Conserva
  USA
   98121
   US-08-975-316-45
  COUNTRY:
  STATE:
  TYPE: DNA
         Matches
  QQ
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  QQ
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   Gaps
   ;
0
  Sequence 9, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: THE MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
   Score 19; DB 2; Length 624;
  Length 624;
   0; Indels
  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
  Pred. No. 1.7
Mismatches
   11000/1003C1
  Score 19;
Pred. No.
   11000.1003
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
   REFERENCE/DOCKET NUMBER: 31,000;
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0563
TELEFAX: 206-269-0563
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTER STILES:
LENGTH: 624 base pairs
TYPE: nucleic acid
STRANBEDNESS: single
TOPOLOGY: linear
US-08-713-000-9
   Query Match 5.3%; Sc
Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
   NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION
TELEPHONE: 206-269-0565
  5.3%; S
100.0%;
  IBM Compatible
  SEQUENCE CHARACTERISTICS:
LENGTH: 624 base pairs
   INFORMATION FOR SEQ ID NO:
  TELEFAX: 206-269-0563
   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
  TYPE: nucleic acid
STRANDEDNESS: single
  CLASSIFICATION: 800
   linear
   Best Local Similarity
   Seattle
  USA
   FILING DATE:
   98121
   COMPUTER:
   ; TOPOLOGY:
US-08-975-316-9
  COUNTRY:
   US-08-975-316-9
   STATE:
  Query Match
  δy
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   Gaps
Gaps
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   Sequence 45, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GEIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
  US-09-211-710-9

US-09-211-710-9

Sequence 9, Application US/09211710A

Patent No. 6204434

GENERAL INFORMATION:

APPLICANT: Bloksberg, Leonard N.

APPLICANT: Bloksberg, Leonard N.

TITLE OF INVENTION: Materials and Methods for the

TITLE OF INVENTION: Modification of Plant Lignin Content;

TITLE REFERENCE: 11000.1003c31

CURRENT APPLICATION NUMBER: US/09/211,710A

CURRENT FILING DATE: 1998-12-14

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 9

LENGTH: 624
   DB 4; Length 624;
1.7;
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   ö
   Gaps
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   5.3%; Score 19; DB 3; Length 1344;
100.0%; Pred. No. 1.7;
   Length 684;
   0; Indels
   0; Indels
   US-08-705-771-8
Sequence 8, Application US/08705771
Patent No. 6054289
GENERAL INFORMATION:
APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
APPLICANT: Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
TITLE OF INVENTION: Expression Products
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
   Query Match 5.3%; Score 19; DB 2; Best Local Similarity 100.0%; Pred. No. 1.7; Matches 19; Conservative 0; Mismatches (
  ATTORNEY AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
  ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
   Mismatches
  APPLICATION NUMBER: US/08/705,771
FILING DATE: August 30, 1996
CLASSIFICATION: 536
   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
   5.3%,
100.0%; Pie
  OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1344 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  261 GCTGGGCGTGCTGGCTGAG 279
  326 ggaggagggagggaa 344
  959 GGAGGAGGGAGGGAA 977
  169 gctgggcgtgctggctgag 187
  SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   19; Conservative
                                      INFORMATION FOR SEQ ID NO:
   973-994-1744
TELEFAX: 206-269-0563
   ROSELAND
NEW JERSEY
  ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-705-771-8
   Best Local Similarity
   linear
   USA
   COUNTRY: US
   ; TOPOLOGY:
US-08-975-316-45
   Query Match
   Matches
  рp
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Gaps
  ;
0
   US-08-765-662-13
Sequence 13, Application US/08765662
Patent No. 5929213
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 14
STREET: ASSESSE: Fish & Richardson
STREET: La Jolla
  Query Match 5.0%; Score 18; DB 4; Length 2407; Best Local Similarity 100.0%; Pred. No. 5.5; Matches 18; Conservative 0; Mismatches 0; Indels
   38,347
ER: 07265/042WOl (FD-3830)
  GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Railos, S. Carl
APPLICANT: Railos, S. Carl
APPLICANT: Railos, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, Hajime
TITLE OF INVENTION: N-End Rule Pathway Enzymes
FILE REFERENCE: BB-1199
CURRENT APPLICATION NUMBER: US/09/370,807
CURRENT FILING DATE: 1999-08-09
EARLIER FILING DATE: 1999-08-09
BARLIER FILING DATE: 4 Mqust 12, 1998
NUMBER OF EGG ID NOS: 16
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
LENGTH: 2407
   OPERATING SYSTEM: DOS
SOFTWARE: FastSED Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,662
FILING DATE: 28-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
                           Sequence 7, Application US/09370807
Patent No. 6297034
   TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
   13:
   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
  513 GCTTTGCAGCAATAACTG 496
  SEQUENCE CHARACTERISTICS:
LENGTH: 2419 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   50 gctttgcagcaataactg 67
   INFORMATION FOR SEQ ID NO:
  ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
   TELEFAX: 619-678-5099
  ; ORGANISM: Oryza sativa US-09-370-807-7
  USA
  CA
US-09-370-807-7/c
  COUNTRY:
   CITY: STATE:
  TYPE: DNA
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Sequence 1, Application US/09173914

Sequence 1, Application US/09173914

Sequence 1, Application US/09173914

Patent No. 6171857

GENERAL INFORMATION:

APPLICANT: Hendrickson, Eric

TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and

TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity

TITLE OF INVENTION: MOMBER: US/09/173,914

CURRENT FILING DATE: 1997-10-16

EARLIER PPLICATION NUMBER: 60/064,557

EARLIER PILING DATE: 1997-10-17

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1

LENGTH: 6078
   Gaps
           Gaps
           ö
   ;
0
   Sequence 1, Application US/08483376;
Sequence 1, Application US/08483376;
Patent No. 595530
GENERAL INFORMATION:
APPLICANT: Vasil, vimla
APPLICANT: Clancy, Maureen A.
APPLICANT: Vasil, Indra K.
APPLICANT: Hannah, L. C.
TITLE OF INVENTION: No. 5955330el Means for Enhancing General Expression
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
   Query Match 5.0%; Score 18; DB 4; Length 6078; Best Local Similarity 100.0%; Pred. No. 5.6; Matches 18; Conservative 0; Mismatches 0; Indels
           0; Indels
           Mismatches
         ö
   330 gagggagggagggagga 347
   204 gagggagggagggaagga 221
       18; Conservative
  ; LOCATION: (1014)...(1014)
US-09-173-914-1
   ..(453)
   ..(610)
  (178)...(178)
   ..(473)
  ..(612)
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ORGANISM: Homo Sapiens
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   Οy
  ó
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0
  Sequence 13, Application PC/TUS9508745
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
  5.0%; Score 18; DB 2; Length 2419;
100.0%; Pred. No. 5.5;
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  5.0%; Score 18; DB 5; 100.0%; Pred. No. 5.5;
  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATING SYSTEM:
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: 12-JUL-1995
CLASSIFICATION:
   ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPHONE: 619-678-5070
  INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2419 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-765-662-13
  NAME/KEY: Coding Sequence

COCATION: 218...1267

COTHER INFORMATION:

PCT-US95-08745-13
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  329 ggagggagggaggaagg 346
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/483,376
FILING DATE: 07-JUN-1995
PRIOR APPLICATION UNMBER: US/08/418,540
FILING DATE: 07-APR-1995
PRIOR APPLICATION NUMBER: US/08/418,540
FILING DATE: 07-APR-1995
PRIOR APPLICATION NUMBER: US/08/102,115
APPLICATION NUMBER: US/08/102,115
APPLICATION NUMBER: US/08/103,956
FILING DATE: 04-AUG-1993
PRIOR APPLICATION NUMBER: US/07/830,956
FILING DATE: US-FEB-1992
PRIOR APPLICATION NUMBER: 10-94B
FILING DATE: 18*MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: FETDER UNMBER: 33,878
REFERENCE/DOCKET NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 10-94B
TELEPAX: (303) 499-8089
INFORMATION FOR EQUID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6386 base pairs
TELENGTH: 6386 base pairs
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INFORMATION FOR EQUID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6386 base pairs
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TTPEL CHARACTERISTICS:
LENGTH: G386 base pairs
TOPOLLOGY: linear
ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle, Suite 201
   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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STRAIN: Black Sweet
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STATE: Colorado
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  COUNTRY:
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   ö
   GENERAL INCORDINGS

APPLICANT: Soreq, Hermona
APPLICANT: Sareq, Hermona
APPLICANT: Shain
APPLICANT: Shain
APPLICANT: Shain
APPLICANT: Shain
APPLICANT: Shain
APPLICANT: Shain
APPLICANT: Shain
APPLICANT: Shain
APPLICANT: Shain
ADPLICANT: Shain
ANDRESS: 7
CORRESPONDENCE ADDRESS: 7
STREET: 30500 No. 602183thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
  Query Match 5.0%; Score 18; DB 2; Length 6386; Best Local Similarity 100.0%; Pred. No. 5.6; Matches 18; Conservative 0; Mismatches 0; Indels
  ZIP: 4834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
  REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
TELEPAX: (248) 539-5056
TELEPAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
   RESULT 37
US-08-814-095-7/c
; Sequence 7, Application US/08814095
; Patent No. 6025183
   ATTORNEY AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
   SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
  325 tggaggaggaggaggg 342
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TOPOLOGY: linear

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  ORGANISM: Homo sapiens
POSITION IN GENOME:
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   NAME/KEY: exon
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US-08-814-095-7
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```
APPLICANT: BRECHOT, Christian
APPLICANT: WANG, Jian
APPLICANT: CHENIVESSE, Xavier
  Db 1165 CAGCAATAACTGATGGC 1149
  MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
   56 cagcaataactgatggc 72
   Best Local Similarity 100.
Matches 17; Conservative
  single
   CORRESPONDENCE ADDRESS:
  nucleic acid
   COUNTRY: USA
  ALDANA
STREET: 727 IWENCE
CITY: Arlington
STATE: Virginia
   linear
   Arlington
  TYPE: nucleic
STRANDEDNESS:
   22202
  US-09-210-889-1/c
   NAME/KEY:
  CCATION:
COCATION:
US-08-460-895-1
   TOPOLOGY:
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5.0%; Score 18; DB 3; Length 35060; 100.0%; Pred. No. 5.7; tive 0; Mismatches 0; Indels
  Length 217;
   Indels
   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
  Sequence 4, Application US/08332766A
; Sequence 4, Application US/08332766A
; Patent No. 2843647;
; GERREAL INFORMATION:
APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
TITLE OF INTENTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
  REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB TELECOMMUNICATION INFORMATION:
  4.8%; Score 17; DB 2;
100.0%; Pred. No. 17;
tive 0; Mismatches
   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 28 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
   RESULT 39
US-08-460-895-1/C
; Sequence 1, Application US/08460895
; Patent No. 5849508
; PATENT INFORMATION:
; APPLICANT: BRECHOT, Christian
   APPLICANT: BRECHOT, Christian APPLICANT: WANG, Jian
  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
   Db 23954 GAGGGAGGGAGGAAGGA 23937
  TELEPHONE: (202) 861-3000
TELEFAX: (202) 862-9944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
  330 gagggagggagggagga 347
   Floppy disk
   331 agggagggagggaagga 347
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nucleic acid
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   102 AGGGAGGGAGGAAGGA 86
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Best Local Similarity 100.0
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   δλ
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APPLICANT: CHRIVESSE, XAULET
PROJUCANT: 2107F; "d first betabled
TAPLICANT: Taplicant Taplican
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; TOPOLOGY: linear
US-08-692-787-8
  linear
   Houston
   STATE: 1c...
COUNTRY: USA
77210
  STRANDEDNESS:
  Texas
  USA
   US-09-097-199-8/C
  ò
   δ
   ö
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   Score 17; DB 3; Length 1634;
  Sequence 8, Application US/08692787
Patent No. 5882864
GENERAL INFORMATION:
APPLICANT: A. Gang
APPLICANT: Ralph, David
APPLICANT: Relph, David
APPLICANT: Relph, David
APPLICANT: NCOBET
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE
NUMBER OF SEQUENCES: 82
  Human cyclin A coding sequence from base 97 to base 1392, coding for a protein of 432 amino acids.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 500 Kb storage COMPUTER: IBM PC/XY/AT or compatibles
OPERATING SYSTEM: MS-DOS version 3.0 or above SOFTWARE: WORD PERFECT 5.1
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Matches 17; Conservative 0; Mismatches
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/650, 805
FILING DATE: 06-FEB-1991
APPLICATION NUMBER: FF9001596
FILING DATE: 12-FEB-1990
INFORMATION FOR SEQ ID NO: 1 :
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   APPLICATION NUMBER: US/08/692,787
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,889
   ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
   COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  NAME: Corder, Timothy S. REGISTRATION NUMBER: 38,414
REFERENCE/DOCKET NUMBER: UROC:012
TELECOMMUNICATION INFORMATION:
  Db 1165 CAGCAATAACTGATGGC 1149
   ATTORNEY/AGENT INFORMATION:
   56 cagcaataactgatggc 72
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  CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
   CDNA
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ORIGINAL SOURCE:
  Houston
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  NAME/KEY:
   US-09-210-889-1
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   ò
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ö
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   GENERAL INFORMATION:

APPLICANT: An, Gang
APPLICANT: O'Hara, S. Mark
APPLICANT: Ralph, David
APPLICANT: Ralph, David
APPLICANT: Neltri, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSE: ANDLAGS
STREET: P.O. BOX 4433
  ö
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0
  Ouery Match

4.8%; Score 17; DB 2; Length 1649;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels
  4.8%; Score 17; DB 4; Length 1649;
100.0%; Pred. No. 17;
Live 0; Mismatches 0; Indels
  CURRENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
FILING DATE:
CLASSICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,787
FILING DATE:
NAMME: NAKASHIMA, RICHARD
NAME: NAKASHIMA, RICHARD
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:018
TELECOMMUNICATION INFORMATION:
   ; Sequence 8, Application US/09097199
; Patent No. 6218529
TELEPHONE: (512) 418-3000
TELERAX: (512) 474-7577
INPORMATION FOR SEG ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 1649 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
   TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
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TYPE: nucleic acid
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Matches 17; Conservative
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  ö
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  Sequence 14, Application US/09109663

Patent No. 6277981

GENERAL INFORMATION:

APPLICANT: Tu, Guang-Chou

APPLICANT: Israel, Yedy

TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF

TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES

FILE REFERENCE: 9855-301
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   4.8%; Score 17; DB 4; Length 80246; 100.0%; Pred. No. 19; tive 0; Mismatches 0; Indels (
   Sequence 3, Application US/09078294
Patent No. 6265211
GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Michael R.
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION UNMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOUTHARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 80595
   APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A MOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER: OF SEQ. ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
  ; TYPE: DNA
; ORGANISM: Nucleotide sequence of HC-contig
US-09-078-294-3
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US-09-078-294-4
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CURRENT APPLICATION NUMBER: US/09/109,663
CURRENT FILING DATE: 1998-07-03
EARLIER APPLICATION NUMBER: 60/051,705
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PATENTIN VET. 2.0
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  TYPE: DNA
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

September 20, 2002, 04:07:18 ; search time 3900.56 Seconds (without alignments) 1235.313 Million cell updates/sec Run on:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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gb\_estl:\* em\_estba:\* 55... 1111... 112... 115... 115... Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_gss\_vrt:\*

SUMMARIES

|   | Description              |                   | AU135588 AU135588 | BG384217 303216 MA | AQ508395 RPCI-11-2 | Z44377 HSC1ZB081 n | AQ528018 RPCI-11-3 | AG163359 Pan trogl | AI394181 tg67a04.x | B20638 F15016-T7 I | BE050974 za71c12.g | BH293527 CH230-30L | BF592428 7156a03.x | R11136 yf39b09.rl | AI481405 vg17d11.x | BE050973 za71c12.b | AZ654841 1M0529P18 | BH337839 CH230-194 | BM310687 ig47b12.y |
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|   | Query<br>Match Length DB | 1                 | 736               | 535                | 158                | 292                | 709                | 716                | 401                | 827                | 282                | 309                | 371                | 406               | 465                | 478                | 483                | 515                | 523                |
| ф | Query                    | 1 1 1 1 1         | 14.3              | 10.9               | 6.7                | 6.7                | 6.7                | 6.7                | 6.4                | 6.4                | 6.2                | 6.2                | 6.3                | 6.2               | 6.2                | 6.2                | 6.2                | 6.2                | 6.2                |
|   | Score                    | 1 1 1 1 1 1       | 51                | 39                 | 24                 | 24                 | 24                 | 24                 | 23                 | 23                 | 22                 | 22                 | 22                 | 22                | 22                 | 22                 | 22                 | 22                 | 22                 |
|   | Result<br>No.            | 1 1 1 1 1 1 1 1 1 | 1                 | 2                  | m                  | 7                  | 0                  | و<br>د             | 7                  | в<br>С             | ٥<br>د             | 10                 | c 11               | 12                | c 13               | c 14               | c 15               | c 16               | c 17               |

| 6.2 525 12 AZ647100 AZ6471<br>6.2 544 12 AQ415718 AQ4157<br>6.2 559 12 AQ78910 AQ778<br>6.2 572 12 AZ378099 AZ378<br>6.2 591 12 AZ378099 AZ378<br>6.2 591 12 AZ388464 AZ8284<br>6.2 615 12 AQ924975 BT0930 BT0938 | 6.2 713 12 A2742461 A2742461 6.2 754 12 AQ983682 A2742461 AQ983682 6.2 760 10 BEB77424 BEB777424 BEB777424 BEB777424 BEB777424 BEB777424 BEB777424 BEB777424 BEB777424 BEB7774281 BGB723588 BGB73833 BGB7378 | 99 99 99 99 99 99 99 99 99 99 99 99 99  | 5.9 212 12 AZ656509 AZ6565<br>5.9 269 10 F11105 F1110<br>5.9 294 12 AZ553751 AZ5537<br>5.9 319 12 B50482 B50482  ALIGNMENTS |                                                                          | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (base; 1 to 736)  Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T. Mar human cDNA project  Unpublished (2000) | enonics Laboratory 532-3 Yana, Kisarazu, C el: 814.48-52-3951 ax: 81-438-52-3952 axi: 81-438-52-3953 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-3952 axi: 91-438-52-52-52 axi: 91-438-52-52 axi: 91-438-52 axi: 91-438-52 axi: 91-438-52 axi: 91-438-52 axi: 91-438-52 axi: 91-438-52 axi: 91-438-52 a | /NOLE="Vector: pminoships"<br>163 a 199 c 199 g 170 t 5 others |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------|-----------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|
|                                                                                                                                                                                                                   |                                                                                                                                                                                                              | 2 w w w w w w w w w w w w w w w w w w w | •                                                                                                                           | - Z - X                                                                  | CE RS                                                                                                                                                                                                                                                                                                                                                                                                         | GATURES SOURCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | BASE COUNT<br>ORIGIN                                           |
| 0000000                                                                                                                                                                                                           | υυ                                                                                                                                                                                                           | υυυυ                                    | υυ                                                                                                                          | AU13588 LOCUS LOCUS DEFINITIC ACCESSION VERSION KEYWORDS SOURCE OORGANIS | REFEREN<br>AUTHO<br>TITLE<br>JOURN<br>COMMENT                                                                                                                                                                                                                                                                                                                                                                 | FEAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | BASE                                                           |

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   Matches
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  MEDLINE
COMMENT
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GSS.
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GSS.
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PCR PRIMERS
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Reele, J.W.
   Design and use of two pooled tissue normalized cDNA libraries for Ext discovery in swine Unpublished (2000)
Contact: Smith TPL
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  .;
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               Length 736;
   ысэвч217
303216 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BG384217
  0; Indels
  USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4399 Email: smith@email.marc.usda.gov
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100.0%; Pred. No. 1.8e-14;
Live 0; Mismatches 0;
   DB 10; I
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292 bp mRNA linear EST 14-NOV-1994 HSCLZBO81 normalized infant brain cDNA Homo saplens cDNA clone 212D08, mRNA sequence.
   ó
   library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACRC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@tesgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: SP6 Carles: BAC ends.
  Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Eorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A. IMAGE: molecular integration of the analysis of the human genome and its expression
      Chordata; Craniata; Vertebrata; Euteleostomi;
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Clones are derived from the human BAC library RPCI-11. For BAC
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                              Primates; Catarrhini; Hominidae; Homo
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  Unpublished (1997)
Other GSSs: RPCI-11-274EIL.TV
Other GSSs: RPCI-11-274EIL.TV
Contact: Shaying Taho, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
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Mammalia; Eutheria;
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lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
87 c 86 g 56 t 3 others
   πασυσυμα 109 bp DNA linear GSS 18-MAY-1999 RPCI-11-313F19.TV RPCI-11 Homo sapiens genomic clone RPCI-11-313F19
   ö
   library availability, please contact Pieter de Jong Pieterdedoron, une de Luffalo.edu. Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seg primer: T7 class: BAC ends.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 709)
   Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
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  Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
  Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
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Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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tive 0; Mismatches 0; Indels
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Ochter_Bhaying Labo, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
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   ORIGIN
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   ŏ
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Location/Qualifiers

FEATURES

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Cabese, I. 10 740; M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, WE:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
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RPCII1 Human Male BAC Library"

RPCII1 Human Male BAC Library"
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  GSS 09-JAN-2002
  ö
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GSS; GSS (genome survey sequence).
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Pan troglodytes
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   RESULT
   LOCUS
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  g
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   FEATURES
   TITLE
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  COMMENT
   RESULT
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//hote="Organ: mixed pooled properties"
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reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I. M.A.G.E. clones 260232-265223,
340488-34479, and 484488-489479."
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 401)
   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
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24; Conservative
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   1 (bases 1 to 282)
O'Shaughnessy,A.L., Habermann,K., de la Bastide,M., Huang,E.N.,
Nascimento.L.U. Schutz,K., Matero,A., Swaby,I., See,L.-H., Preston
,R.R., Rodriguez,M.A., Shah,R.S., Shekher,M., Spiegel,L.A., Vil
,M.D., Dedhia,N.N. and McCombie,W.R.
Expressed sequence tags from Zea mays (maize)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosida; II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 827)
Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and
   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade, Panicoideae, Andropogoneae, 2ea.
   /note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
   Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
   Gaps
   ö
   6.4%; Score 23; DB 12; Length 827;
100.0%; Pred. No. 1.4;
Live 0; Mismatches 0; Indels
  23 others
  Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
Cold Spring Harbor Laboratory
Po Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8874
Email: mccombie/ecshl.org
Plate: 2a71 row: c column: 12
Seq primer: -40Ml3RevUniv
   /organism="Arabidopsis thaliana"
  284 t
  Email: jecker@atgenome.bio.upenn.edu
Seg primer: T7
Class: BAC ends
   Produced by Thomas Altmann"
233 c 90 g 284 t
  Contact: Ecker J. Arabidopsis Thaliana Genome Center University of Pennsylvania
   High quality sequence start: 175
High quality sequence stop: 226.
Location/Qualifiers
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   /strain-"Columbia
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Unpublished (1997)
Other_GSSs: F15016-Sp6
   /clone_lib="IGF"
  327 gaggaggaggaggaaggaag 349
   /clone="F15016"
   Tel: 215-898-9384
Fax: 215-898-8780
  23; Conservative
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```
Email: szhaoetigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact pleter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 30 row: L. column: 8
Seq primer: T7
Class: BAC ends.
  Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other_GSSs: CH230-30L8.TJ
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CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
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(H230-30L8, TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-30L8, DNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Gaps
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
   ;
0
   DB 9; Length 282; 3.9;
   9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
   0; Indels
  /clone_lib="CHORI-230 Segment 1"
   /organism="Rattus norvegicus"
   48 t
   0; Mismatches
  Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
   /strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-30L8"
   6.2%; Score 22; 100.0%; Pred. No.
High quality sequence stop: 282
  Location/Qualifiers
   86 9
   Location/Qualifiers
   75 g
  329 ggagggaggagggaaggaagc 350
  Pieter de Jong"
   50 GGAGGGAGGGAGGAAGC 29
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   (bases 1 to 309)
  36 c
   123 c
  Query Match
Best Local Similarity 100...
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   36 a
  Rattus.
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   ORGANISM
   BASE COUNT
  ACCESSION
   REFERENCE
   AUTHORS
   JOURNAL
  RESULT 1
BH293527
  FEATURES
   FEATURES
   KEYWORDS
  TITLE
   COMMENT
   SOURCE
  ò
```

```
Contract: Nobert Strausberg, Ph.D.
Contract: Robert Strausberg, Ph.D.
Tissue Procurement: Dennis Sgroi, M.D., Kristina Cole, M.D., Ph.D.
student, Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40RP from Gibco.
  /note="Organ: breast; Vector: pAMP1; mRNA made from breast carcinoma tissue, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 400 bp. Primary library, non-amplified.
  LOCUS R11136 406 bp mRNA linear EST 11-APR-1995
DEFINITION yf39b09.rl Soares fetal liver spleen lNFLS Homo sapiens CDNA clone
   ö
  ö
  EST 12-DEC-2000
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
  7155a03.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338668 3' similar to contains element TARI TARI repetitive element ;, mRNA
  1 (bases 1 to 371)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
   Gaps
  Gaps
   .;
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  DB 12; Length 309; 3.9;
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/lab_host="DH10B"
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/clone="Inge:3338668"
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  Location/Qualifiers
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  328 aggagggagggaggaaggaag 349
  278 AGGAGGGAGGGAAGGAAG 299
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   184 c
  Tumor Gene Index
Unpublished (1997)
  Homo sapiens
   ø
  sequence.
BF592428
   BF592428
  human.
  source
   BASE COUNT
ORIGIN
  12
   DEFINITION
   RESULT 11
   BF592428/c
   ORGANISM
   ACCESSION
  REFERENCE
  AUTHORS
  JOURNAL
  KEYWORDS
  FEATURES
  TITLE
   COMMENT
  RESULT
  VERSION
  g
   ð
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SOURCE ORGANISM

KEYWORDS

VERSION

REFERENCE AUTHORS

ACCESSION

TITLE JOURNAL COMMENT

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1 (bases 1 to 478)
O'Shaughnessy, A.L., Habermann, K., de la Bastide, M., Huang, E.N.,
Nascimento, L.U., Schutz, K., Matero, A., Swaby, I., See, L.-H., Preston
'R.R., Rodriguez, M.A., Shah, R.S., Shekher, M., Spiegel, L.A., Vil
'M.D., Dedhia, N.N. and McCombie, W.R.
Expressed sequence tags from Zea mays (maize)
         1 (bases 1 to 465)
Marra,M., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
   3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; 2ea.
   478 bp mRNA linear EST 08-JUN-200 za71c12.b50 Maize Glume cDNAs Library Zea mays cDNA clone za71c12 BE050973
   4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:505709
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 440.
Location/Qualifiers
   Score 22; DB 9; Length 465;
   0; Indels
   Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
   Washington University School of Medicine
  /clone_lib="Soares mouse NbMH"
/sex="male"
/tissue_type="heart"
/dev_stage="4_weeks"
/lab_host="DHIOB"
  100.0%; Pred. No. 4.1;
tive 0; Mismatches
  114 t
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  /db_xref="taxon:10090"
/clone="IMAGE:861621"
  93 g
  /strain="C57BL/6J
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   63 AGGAGGGAGGGAAGGAAG 42
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Matches 22; Conservative
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  106 a
   Zea mays.
   Zea mays
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BE050973/c
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  TITLE
JOURNAL
  BASE COUNT
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            REFERENCE
  ACCESSION
   REFERENCE
   AUTHORS
  FEATURES
  KEYWORDS
  COMMENT
  TITLE
  VERSION
   ORIGIN
   SOURCE
   οy
   g
   (bases 1 to 406)

Hillar, C., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lemon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston Tr., R. Williamson, A., Wohldmann, P. and Wilson, R. Washu-Merck, EST Project Unpublished (1995)
  465 bp mRNA linear EST 09-MAR-1999 v17dll.x1 Soares mouse NbMH Mus musculus cbNA clone IMAGE:861621 3', mRNA sequence.
IMAGE:129209 5' similar to gb:L21696_cds1 PROTHYMOSIN ALPHA (HUMAN ):contains MER22 repetitive element ;, mRNA sequence.
   ö
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  Email: est@watson.wustl.edu
Insert Size: 2665
High quality sequence stops: 290 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Lengh: 2665 Std Brror: 0.00
Seq primer: M13RPl
High quality sequence stop: 290.
   0; Gaps
   Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
   6.2%; Score 22; DB 10; Length 406;
  0; Indels
  Pred. No. 4.1;
0; Mismatches
  328 aggaggagggagggaag 349
   356 AGGAGGGAGGGAGGAAGGAAG 377
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  100.0%;
  R11136.1 GI:763871
   22; Conservative
  1. 406
   Homo sapiens
   Best Local Similarity
  Mus musculus
  house mouse.
   ď
   101
  human.
```

source

FEATURES

EST 08-JUN-2000

ö

Gaps ö

Query Match

Matches

ô g

BASE COUNT

ORIGIN

DEFINITION

ACCESSION VERSION KEYWORDS

AI481405/c

RESULT 13

ORGANISM

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
                  /sex="Male"
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   BH337839
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   Rattus.
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JOURNAL
COMMENT
   ACCESSION
   REFERENCE
  AUTHORS
   VERSION
KEYWORDS
   FEATURES
   ORIGIN
  SOURCE
  δλ
   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
   ö
   AZ654841 483 bp DNA linear GSS 14-DEC-2000
IM0529918F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 483)
   /note="Vector: Lambda Zap II (Strategene); Site_1: XhOI;
Site_2: EcoRI; Resistance: Ampicillin Autoexcision:
pBluescript SK (+/-) Titer: 7 x 10e-9 pfu/mL (as of
   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
   Gaps
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/clone_lib="Maize Glume cDNAs Library"
Unpublished (2000)
Contact: W. Richard McCombie
Contact: W. Richard McCombie
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tal: 516 367 8884
Fax: 516 367 8874
  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: P column: 18
Seq primer: CGTTGTAAAACGACGCCAGT
   92 t
  clone UUGC1M0529P18 F, DNA sequence.
  Query Match
Best Local Similarity 100.0%; Pred. No. 4.1
  /organism="Mus musculus"
/strain="C57BL/6J"
  Email: mccombie@cshl.org
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High quality sequence stop: 478.
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170 c 127 g
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   AZ654841.1 GI:11791987
   Class: plasmid ends
   Tel: 801 585 5606
Fax: 801 585 7177
  1. .478
  1. 483
  Mus musculus
  house mouse.
   USA
  AZ654841
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   GSS.
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   BASE COUNT
ORIGIN
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  JOURNAL
   REFERENCE
   AUTHORS
   JOURNAL
   KEYWORDS
  FEATURES
   FEATURES
   TITLE
   VERSION
  COMMENT
                      COMMENT
  SOURCE
  qq
```

```
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with THA DNA polymerase and THA polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gil4722114|gb|AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
  Theorem 1 (bases 1 to 515)

Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other_GSSs: CH230-19479.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
  Email: Szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 194 row: J column: 9
Seq primer: T7
Class: BAC ends.
  ö
  GSS 03-DEC-2001
  515 bp DNA linear GSS 03-DEC-2001
CH230-194J9, DNA sequence.
  Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
  Gaps
  ö
  Query Match 6.2%; Score 22; DB 12; Length 483; Best Local Similarity 100.0%; Pred. No. 4.1; Matches 22; Conservative 0; Mismatches 0; Indels
   9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
   Laboratory Mouse DNA Resource
   The Institute for Genomic Research
  Location/Qualifiers
1. .515
  BH337839.1 GI:17268573
```

à Д

```
109 a
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   source
  DEFINITION
  RESULT 18
AZ647100/c
                           BASE COUNT
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  ACCESSION
   VERSION
KEYWORDS
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  AUTHORS
  JOURNAL
  FEATURES
   TITLE
   COMMENT
   ORIGIN
  SOURCE
   LOCUS
   g
  ò
   ·
0
  EST 03-JAN-2002
   //note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1: Site_2: XhoI; CDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional clouhng.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab). Washington University
School of Medicine, Box 8127, 660 South Buclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
  Eukaryotani Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dass 1 to 523)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Leafishka, T., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wille, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Endocrine, Pancreas Consortium
         /strain="mosswiad/wdw"
/db_xref="taxon:10116"
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/clone="cH30-194J9"
/sex="Female"
/sex="Female"
/sex="Ype="Brain"
/note="Vector: pTaRBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
pieter de Jong"
  Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
   Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
   Gaps
  Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
  1947b12.yl HR85 islet Homo saplens cDNA 5', mRNA sequence. BM310687
   ;
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/lab_host="DH10B"
/organism="Rattus norvegicus"
  Pred. No. 4.2;
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Best Local Similarity 100.0%; Pred. No. 4.2
   Seq primer: -40RP from Gibco
High quality sequence stop: 488.
   ,90 g
  Location/Qualifiers
   243 GGAGGAGGAGGAAGGA 222
   326 ддаддадддадддадддадда 347
  BM310687.1 GI:18045003
   Unpublished (2000)
Other_ESTs: ig47b12.x1
   (hinoue@im.wustl.edu)
   154 c
  rel: 617-495-1812
  Fax: 617-495-8557
  Homo sapiens
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   source
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  ORGANISM
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  TITLE
JOURNAL
   REFERENCE
   KEYWORDS
  FEATURES
   VERSION
   COMMENT
  ORIGIN
   SOURCE
  rocus
```

```
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil473214 gbplAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
   GSS 14-DEC-2000
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  ALOW 1100 525 bp DNA linear GSS 14-DEC-200 1M0513122F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0513L22 F, DNA sequence.
   1 (bases 1 to 525)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
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  Email: ddunn@genetics.utah.edu
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  ACCESSION
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   AUTHORS
   JOURNAL
  VERSION
KEYWORDS
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SOURCE
   FEATURES
   TITLE
  COMMENT
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   VERSION
  ORIGIN
  SOURCE
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RPCI-11-204G24.TV RPCI-11 Homo sapiens genomic clone RPCI-11-204G24
   ;
0
chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." 156\ c 91 g 183\ t
   Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
thtp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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Other GSSs: RPCI-11-204624.TJ
Other GSSs: RPCI-11-204624.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
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Triticeae; Hordeum.
1 (bases 1 to 52)
Sato, K., Saisho, D. and Takeda, K.
Unpublished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
  EST 18-JAN-2002
   AQ078910 569 bp DNA linear GSS 20-AUG-1998
CIT-HSP-2367J11.TR CIT-HSP Homo sapiens genomic clone 2367J11, DNA
   ö
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( (bases 1 to 569)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
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  Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 311 838 0200
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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   Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
   Mus musculus sukrayota, Muzaca; Chordata; Craniata; Vertebrata; Euteleostomi; Musmanlia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 572)

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18 (bases 1
  Clones are available from Research Genetics (info@resgen.com). BAC
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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  454 AGGAGGGAGGGAAGGAAG 433
                          Email: mdadams@tigr.org
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   Tel: 801 585 5606
Fax: 801 585 7177
Fax: 301 838 0208
  . 569
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   ಹ
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  BASE COUNT
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q δ

```
(http://www.jax.orgyrescources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qilq/32114|qb)AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
  plasmid inserts
Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
   ö
  AZ828464 591 bp DNA linear GSS 20-FEB-2001
2M0105NJ3F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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0; Mismatches 0; Indels
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100.0%; Pred. No. 4...
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Location/Qualifiers
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   Tel: 801 585 5606
Fax: 801 585 7177
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  COMMENT
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   LOCUS
   ōλ
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   ö
  Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
   Email: szhaoétygr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.bulfalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bulfalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
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   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
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   Conservative
   .615
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   SOURCE
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g δŻ

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Another Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of Control
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  ö
  ó
  Email: maddams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 623)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
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  9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
   Ļ
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Contact: Mark Adams
Contact: Bukaryolic Genomics
The Institute for Genomic Research
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```
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
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Tel: 301 838 0200
Fax: 301 838 0208
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Contact: Shaying Taylog Contact: Shaying Taylog Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA PT: 301 838 0200
    Russell, D., de Jong, P. and Fraser, C.M. Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999)
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   Department of Eukaryotic Genomics
The Institute for Genomic Research
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   Contact: Shaying Zhao
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enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
  BF984535 673 bp mRNA linear EST 23-JAN-2001 602307723F1 NIH_MGC_88 Homo saplens cDNA clone IMAGE:4399276 5',
   ö
   AZ742461 713 bp DNA linear GSS 25-JAN-2001
RPCI-24-74G13.TJ RPCI-24 Mus musculus genomic clone RPCI-24-74G13,
   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I toases I to 713 Jaho, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10102 row: m column: 05
  1 (bases 1 to 673)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
   Gaps
   .;
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   6.2%; Score 22; DB 10; Length 673;
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   Pred. No. 4.3;
   Mismatches
   High quality sequence stop: 671.
Location/Qualifiers
Tissue Procurement: ATCC
   Duery Matcn
Best Local Similarity 100.0%; P
   326 ggaggagggagggaagga 347
   33 GGAGGAGGGAGGGAAGGA 54
  BF984535.1 GI:12387347
  AZ742461
AZ742461.1 GI:12521331
   1. .673
  mRNA sequence.
   DNA sequence.
   Homo sapiens
  Mus musculus
  house mouse.
  BF984535
   AZ742461
  BF98453
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  GSS.
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  JOURNAL
COMMENT
  BASE COUNT
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  RESULT 27
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  REFERENCE
  AUTHORS
  ACCESSION
  KEYWORDS
   REFERENCE
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   FEATURES
  TITLE
   SOURCE
   셤
  ð
   ò
  q
```

```
ö
   AQ983682 73-323.TJ RPCI-23 Mus musculus genomic clone RPCI-23-323J22 DNA sequence.
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pdejong@mail.oho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://ww.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 74 row: G column: 13
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   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
  Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostoni,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 754)
  Gaps
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760 bp mRNA linear EST 20-OCT-2000 601485462F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888134 5', BE877424
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ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BH10B electrocompetent cells (BRL Life Technologies).

a 189 c 131 g 251 t lothers
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/clone_lib="NIH_MGC_69"
/tissue_type="large cell carcinoma, undifferentiated"
/tissue_type="large cell carcinoma, undifferentiated"
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/tissue_libost="lung (page-resistant)"
/note="Organ: lung; Vector: pCWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 323 row: J column: 22 Seq primer: SP6 Class: BAC ends.
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 760)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
  Gaps
  cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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   Indels
  found through the I.M.A.G.E. Consortium/LLNL at:
  ;
0
  100.0%; Prec. ...
  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
   http://image.llnl.gov
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  /organism="Mus musculus"
   /db_xref="taxon:10090"
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  Location/Qualiflers
1. .760
   Location/Qualifiers
1. .754
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   /lab_host="DH10B"
   510 AGGAGGAGGAGGAAGGAAG 489
  328 аддадддадддадддааддаад 349
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   Homo sapiens
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Matches 22; Conserv
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JOURNAL
   ACCESSION
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   AUTHORS
   BE877424
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   COMMENT
   RESULT
   SOURCE
   LOCUS
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õ

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//note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
//note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
//ore="SalI; Cloned unidirectionally."
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602728977F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4868443 5',
mRNA sequence.
   EST 20-0CT-2000
   ö
  ö
  Library constructed by Life
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I thases 1 to 907)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
   BE617281 907 bp mRNA linear EST 20-OCT-2C 601441977F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846235 5',
  CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
tollary sequence start: 8
High quality sequence start: 8
High quality sequence stop: 660.
   Gaps
  Gaps
   ő
  ö
  6.2%; Score 22; DB 10; Length 907;
100.0%; Pred. No. 4.4;
cive 0; Mismatches 0; Indels
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Pred. No. 4.3;
  0; Indels
Average insert size 1.1 kb.
  Mismatches
   Unpublished (1999)
Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
  304 g
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   326 ggaggagggagggagga 347
   326 ggaggaggagggagggagga 347
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  15 GGAGGAGGGAGGGAAGGA 36
   14 GGAGGAGGGAGGGAAGGA 35
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  mRNA sequence.
BE617281
BE617281.1 GI:9888219
  6.2%;
                         Technologies.
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Matches 22; Conservative
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Best Local Similarity
   173 a
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   JOURNAL
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  BE617281
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Fax: 801 585 7177
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  BASE COUNT
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  AUTHORS
   JOURNAL
   FEATURES
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  TITLE
   COMMENT
   ORIGIN
  qq
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   /dlone=TrAAGE:486843"
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/tlsaue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: poTBF; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGGG). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
  1068 bp mRNA linear EST 27-FEB-2001
mRNA sequence.
BG328313
   ö
  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramunal Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnh.gov
Plate: LLCM/38 row: i column: 20
High quality sequence stop: 728.
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1068)
NIH-MCC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 926)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
   Gaps
  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Pragatation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: NIH Intramural Sequencing Center
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  BG328313.1 GI:13134660
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   human.
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   AUTHORS
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                      VERSION
  TITLE
   COMMENT
   SOURCE
   SOURCE
   ð
```

```
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Guiversity of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  2M0280018R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0280018 R, DNA sequence.
   /tissuc_type="adenocarcinoma cell line"
/lab_host="NH10B (phage-resistant,"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oliqo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCAGGGG, size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
294 c 332 g 181 t
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherlia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 43)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Aslam, M., Longarcers, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Clone distribution: MGC clone distribution information can be
   Gaps
   ;
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   Score 22; DB 10; Length 1068;
Pred. No. 4.5;
  0; Indels
                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1233 row: f column: 24
High quality sequence stop: 668.
  Std Error: 0.00
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/clone="IMAGE:4546583"
/clone_lib="NIH_MGC_15"
   High quality sequence stop: 43. Location/Qualifiers
   Email: ddunn@genetics.utah.edu
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ö

us-09-846-456-2.oli.rst

/clone="UUGC1M0090K10"

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source
  BASE COUNT
ORIGIN
  DEFINITION
   35
   ORGANISM
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   JOURNAL
  AZ500262
   FEATURES
  VERSION
  TITLE
  COMMENT
   RESULT
   δ
  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114) [plART29072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
  ;
0
  GSS 29-SEP-2000
  Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I bases 1 to 51)

Dunn,D., Aoyaji,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
  /lab_host="E. coli strain XL10-Gold, T1-resistant, F-" /note="Weetor: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
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  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
  Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 51.
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   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
   /strain="C57BL/6J"
/db_xref="taxon:10090"
  row: K column:
   Location/Qualifiers
  329 ggagggagggagggaag 349
  AZ351915.1 GI:10431152
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                             /sex="Female"
   Tel: 801 585 5606
Fax: 801 585 7177
  Mus musculus
  Plate: 0090
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   source
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AZ351915
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AUTHORS
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KEYWORDS
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  TITLE
  COMMENT
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  SOURCE
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```
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/sex="Male"
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/note="Vector: PWD42nv; Purified genomic DNA from M..
musculus G57BL/6/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch norifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inductible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for amplicillin resistance."
   ΙŢ
  GSS 05-OCT-2000
   ö
  Mus musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 62)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longarce,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
   AZ500262
1M0338H04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0338H04 R, DNA sequence.
   plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 318, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
  Gaps
   ..
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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  Std Error: 0.00
  rel: 801 585 5606
Fax: 801 585 7177
Email: ddunndgenetics.utah.edu
Insert Length: 10000 Std Error: 0.(
Plate: 0338 row: H column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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  AZ500262
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   JOURNAL
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   AUTHORS
   KEYWORDS
   FEATURES
  VERSION
  TITLE
  COMMENT
  ORIGIN
   g
  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 gplAF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
   ö
   GSS 03-OCT-2000
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 66)

Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
   AZ411857 66 bp DNA linear GSS 03-OCT-200
1M0185006F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Weetcn: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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  Email: ddunn@genetics.utah.edu
Insert Length: 10000 std Error: 0.00
Plate: 0185 row: 0 column: 06
Seq primer: CGTTGTAAAACGACGCCCAGT
  clone UUGC1M0185006 F, DNA sequence.
   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
  /ordanism="Mus musculus"
  High quality sequence stop: 66. Location/Qualifiers
  AZ411857.1 GI:10535870
   Class: plasmid ends
   Tel: 801 585 5606
Fax: 801 585 7177
  Mus musculus
  house mouse.
  84112, USA
  AZ411857
  Source
   BASE COUNT
ORIGIN
  DEFINITION
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  ACCESSION
  REFERENCE
  AUTHORS
  JOURNAL
  KEYWORDS
   FEATURES
   TITLE
   VERSION
  COMMENT
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ò g

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLL0-Gold (Stratagene) cells and selected for ampicialin resistance."
  ö
   AZ638528 90 bp DNA linear GSS 20-FEB-2001 2M0134E17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic cone UUGC2M0134E17 F, DNA sequence.
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
   Mammalia; Butheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 90)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
   /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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   Laboratory Mouse DNA Resource
   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0134 row: E column: 17
  24 t
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Class: plasmid ends
High quality sequence stop: 90.
Location/Qualifiers
  Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
/db_xref="taxon:10090"
/clone="UUGC1M0185006"
   AZ838528.1 GI:13008436
  329 ggagggagggagggaaggaag 349
  57 GGAGGGAGGGAGGAAG 37
   /sex="Male"
  37 C
  Tel: 801 585 5606
Fax: 801 585 7177
   Mus musculus
  house mouse.
  AZ838528
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ORIGIN
  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high monar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114 qib1AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus.
1 (bases 1 to 120)
2 hao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Nouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
   ö
  AZ743191 120 bp DNA linear GSS 25-JAN-2001
RPCI-24-146C22.TJ RPCI-24 Mus musculus genomic clone RPCI-24-146C22
   Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
agge: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 146 row: C column: 22
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Matches 21; Conserv
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  Query Match
  BASE COUNT
  RESULT 38
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   ACCESSION
  JOURNAL
   REFERENCE
  VERSION
KEYWORDS
   AUTHORS
   AZ743191
   TITLE
  ORIGIN
   SOURCE
```

ολ

```
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissaue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael
R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrpy/image.html
Seq primer: -40ml3 fwd.ET from Amersham.
  AI053852 15-JUL-1998
qi70c08.xl NCI_CGAP_Ov26 Homo sapiens cDNA clone IMAGE:1861838 3'
similar to contains element TARI TARI repetitive element ;, mRNA
  ö
  /cell_type="Spleen/Brain" /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; Anote="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male CS/BL/6J DNA."
  /note="Organ: ovary; Vector: pAMP1; mRNA made from papillary serous ovarian carcinoma, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified.
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 145)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Taxional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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100.0%; Pred. No. 11.
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1. .145
Location/Qualifiers
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  84 GGAGGGAGGGAGGAAG 104
   /sex="female"
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AI053852.1 GI:3321639
   /sex="Male"
   16 c
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  Homo sapiens
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Best Local Similarity
  ø
   42 a
  sednence.
  human.
                             source
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  AI053852/c
  ORGANISM
   BASE COUNT
   BASE COUNT
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  Matches
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   JOURNAL
  REFERENCE
  AUTHORS
   KEYWORDS
  FEATURES
  FEATURES
   /ERSION
  TITLE
   COMMENT
   ORIGIN
  SOURCE
   셤
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Unpublished (2000)
   Conservative
   Tel: 801 585 5606
Fax: 801 585 7177
   Mus musculus
   house mouse.
   Query Match
Best Local Similarity
Matches 21; Conserv
   USA
   84112,
   source
  DEFINITION
   ORGANISM
   BASE COUNT
  ACCESSION
   JOURNAL
   VERSION
KEYWORDS
   REFERENCE
   AUTHORS
                        AZ457379
  FEATURES
   TITLE
  SOURCE
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/db_ref="RPCI-23-7H17"
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/sex="Female"
/lab_host="BH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially disested with a combination of ECORI and ECORI methylase. Size selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
  ;
0
  AZ091117 15 RPCI-23 Mus musculus genomic clone RPCI-23-7H17,
  Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 161)
Loases 1 to 161)
Loarman W. Feldblyum, T., Malek, J., Shatsman, S., Akhinet, J., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akhinet, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-7H17.TV
Contact: Shaying Labo
Department of Eukaryotic Genomics
The Institute for Genomic Research
   ;
0
   Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6
Class: BAC ends.
   Gaps
   Gaps
  ö
   ö
  5.9%; Score 21; DB 12; Length 161;
100.0%; Pred. No. 12;
tive 0; Mismatches 0; Indels
    Length 145;
  0; Indels
   9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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   ORGANISM
   BASE COUNT
   JOURNAL
COMMENT
  ACCESSION
   VERSION
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   REFERENCE
   AUTHORS
  FEATURES
   TITLE
   ORIGIN
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  a
   ô
  g
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAD42 (gil47321141gblAR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
A2457379 191 bp DNA linear GSS 04-0CT-2000 1M0260L10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0260L10 R, DNA sequence.
   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
   ô
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I base; Lto 191)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly and Wright,D.,Weiss,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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//ab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
//ab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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musculus C57BL/6J (male) was obtained from the Jackson
   Gaps
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   Laboratory Mouse DNA Resource
  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0260 row: L column: 10
   Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 191.
Location/Qualifiers
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  AUTHORS
   JOURNAL
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  F11105
  SOURCE
  LOCUS
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  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114(gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
   A2656509 212 bp DNA linear GSS 14-DEC-2000 1M0532002F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0532002 F, DNA sequence.
   308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 212)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Slam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
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  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
  /organism="Mus musculus"
   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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  169 GAGGAGGGAGGGAAGGA 189
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Tel: 801 585 5606
Fax: 801 585 7177
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   source
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  ACCESSION
   REFERENCE
  JOURNAL
   AUTHORS
   KEYWORDS
   FEATURES
   TITLE
  COMMENT
   VERSION
   ORIGIN
   SOURCE
  LOCUS
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0

Gaps

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0; Indels

100.0%; Pred. No. 12; tive 0; Mismatches

Best\_Local Similarity 100. Matches 21; Conservative

329 ggagggagggagggaag 349

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/dev_stage="3 months old"
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isolate=muscular atrophy patient; tissue_type=total brain;
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cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, N.A.S in press" 3 others
  194 bp DNA linear GSS 05-OCT-2000 IM0360B02F Mouse 10kb plasmid UGG1M library Mus musculus genomic clone UGG21M0360B02 F, DNA sequence.
269 bp mRNA linear EST 12-MAR-1995
HSC2TE032 normalized infant brain cDNA Homo sapiens cDNA clone
c-2te03 3', mRNA sequence.
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I bases 1 to 269.

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Sebastiani Kabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
  Email: genexpress@genethon.fr
Single read. 19T removed at sequence 5'end
Genexpress_lbrary_idt. C; Genexpress_sequence_idt: a3c-2te03
Seq primer: (-21)M13_universal.
Location/Qualifiers
  Gaps
  Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995) 95277534
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  Contact: Genethon
   Tel: 33169472800
  Fax: 33160778698
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   ACCESSION
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KEYWORDS
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source
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   BASE COUNT
   JOURNAL
  REFERENCE
   AUTHORS
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   FEATURES
  TITLE
  COMMENT
                                 SOURCE
  ŏ
   (http://www.jax.orgyresources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
  Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
WR. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
   B50482
319 bp DNA linear GSS 20-JUN-1998
CIT-HSP-437M12.TP CIT-HSP Homo sapiens genomic clone 437M12, DNA
sequence.
B50482
B50482.1 GI:2602719
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 294)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Laboratory Mouse DNA Resource
  Mouse whole genome scaffolding with paired end reads from 10kb
  Gaps
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0360B02"
/sex="Male" Mouse 10kb plasmid UUGC1M library"
  Query Match 5.9%; Score 21; DB 12; Length 294; Best Local Similarity 100.0%; Pred. No. 12; Matches 21; Conservative 0; Mismatches 0; Indels
  Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0360 Inw: B column: 02
Seq primer: CGTTGTAAAACGACGCCCAGT
Class: plesmid ends
   High quality sequence stop: 294.
  329 ggagggagggagggaag 349
  Tel: 801 585 5606
Fax: 801 585 7177
  plasmid inserts
                              Mus musculus
  house mouse.
   131
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                      ORGANISM
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  COMMENT
   VERSION
SOURCE
   ò
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  Email: ung@ash.tree.caltech.edu
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: SP6
Class: BAC ends.
   \text{Kim}[U.-J., Adams,M.D. and Simon,M.I. Determination of clone end sequences of human Bacterial Artificial
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Other_GSS: CIT-HSP-437M12.TV
Contact: Ung-Jin Kim
CalTech Genome Research Lab
California Institute of Technology
Division of Biology, MS 147-75, Pasadena, CA 91125, USA
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   Score 21; DB 12; Length 319;
Pred. No. 12;
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  132 t
  Search completed: September 20, 2002, 04:07:24 Job time: 13778 sec
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  /db_xref="taxon:9606"
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  /clone_lib="CIT-HSP"
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Homo sapiens
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Run on:

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September 20, 2002, 06:30:00; Search time 5250.46 Seconds (without alignments) 880.830 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Description

SUMMARIES

Query Score Match Length DB ID

No.

Result

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| C C 336 SOURCES SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE 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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        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                                                                            |                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                               | RESULT<br>AX3510<br>LOCUS<br>DCETNI<br>DCETNI<br>DCETNI<br>VERSIO<br>KEYWOR<br>SOUNCA<br>ORGA<br>AUTH<br>TITL<br>JOUR<br>FEATUR<br>S                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

; 0

0; Gaps

0; Indels

0; Mismatches

Matches 221; Conservative

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 697)

Analysis of Ah8Cl gene 5' end: additional peptide sequence,
Analysis of Ah8Cl gene 5' end: additional peptide sequence,
promoter region, and four polymorphisms

NL Biochem. Biophys. Res. Commun. 271 (2000) In press

Promoter. N. Hakamata, H., Duchateau, D.N., Eng, C.,
Anuizerat. B.E., Fielding, C.J. and Kane, J.P.

Direct Submission

NL Submitted (19-AFR-2000) Cardiovascular Research Institute,
University of California, San Francisco, CA 94143-0130, USA

Location/Oualifiers
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  REFERENCE
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   JOURNAL
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  AUTHORS
  JOURNAL
  gene
   AF258627
   KEYWORDS
   CDS
  FEATURES
  VERSION
  TITLE
   TITLE
   SOURCE
   ORIGIN
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Score 221; DB 9; Length 697; Pred. No. 5.2e-118;

100.0%; 100.0%;

Best Local Similarity

Query Match

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Kaminski, W.B., Decouplik, W., Honer, C., Schumacher, C. and Schmitz, G. The zinc finger protein 202 (znf202) is a transcriptional repressor of atp binding cassette transporter al (abcal) and abcgl gene expression and a modulator of cellular lipid efflux 21192304.
   PRI 10-APR-2001
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1167)
  Direct Submission
Submitted (05-JAN-2000) Porsch-Oezcueruemez M.K., Institute for Clinical Chemistry, Universitiy of Regensburg,
FRanz-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY
Location/Qualifiers
                     61 ccgggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggc 120
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   'function="cholesterol efflux regulatory protein"
   HSA252201 1167 bp DNA linear PRI I Homo sapiens partial ABC-1 gene for ATP-binding cassette transporter-1, 5'UTR and promoter region.
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Porsch-Oezcueruemez, M.K.
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   JOURNAL
   REFERENCE
   AUTHORS
  JOURNAL
   MEDLINE
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   FEATURES
  VERSION
  TITLE
  TITLE
   SOURCE
   ORIGIN
                                  g
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   Qγ
  Ω
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getttgeteettgtttttteeeeggttetgtttteteeectteteeggaaggettgteaa 180

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987 CCGGGCTGCGGCAGGGCAGGGGGGGGGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGC 1046
   121
  TITLE
   SOURCE
  RESULT
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  AFIJUN-2000 HOMO Sapiens ATP binding cassette transporter 1 (ABCA1) gene, promoter and exon 1.
   ö
  Submitted (20-APR-2000) Cardiovascular Research Institute, Oniversity of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 94143-0130, USA (bases 1 to 1167) 
  Submitted (23-JUN-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1167)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P. Analysis of hARCI gene 5' end: additional peptide sequence, promoter region, and four polymorphisms
Biochem. Biophys. Res. Commun. 271 (2000) In press 224 to 1167)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
  1047 GCTTTGCTCCTTGTTTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAA 1106
   gctttgctccttgtttttccccggttctgttttctccccttctccggaaggcttgtcaa 180
  ccgggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggc 120
                                    61 ccgggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggc 120
   0; Gaps
   Sequence update by submitter
On Jun 23, 2000 this sequence version replaced gi:7769713.
Location/Qualifiers
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224 . 844
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  source
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AF258623S1
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ORIGIN
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JOURNAL
   TITLE
JOURNAL
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  AUTHORS
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COMMENT
   JOURNAL
  REFERENCE
  KEYWORDS
   FEATURES
  TITLE
  /ERSION
  SEGMENT
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  PAT 10-OCT-2001
  PAT 06-FEB-2002
  1 (sites)
Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
Enswer,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 1 08-NOV-2001;
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 7260)
Schmitz,G. and Bodžioch,M.
Atp binding cassette transporter 1 (abc1) gene polymorphisms and
uses thereof for the diagnosis and treatment of lipid,
cardiovascular or inflammatory disorders
  2894 GTAATTGCGAGCGAGGGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCTTCTCTC 2953
   2954 ccgggcrgcggcagggcagggcgggagcrccgcgcaccaacaagagccggrrcragggc 3013
   1 gtaattgcgagcgagagtgagtggggccggggacccgcagagccgagccttctctc 60
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   3074 GGGGTAGGAGAAGAGACGCAAACACAAAAGTGGAAAACAG 3114
                   ggggtaggagaaagagacgcaaacacaaaagtggaaaacag 221
181 ggggtaggagaaagagacgcaaacacaaaagtggaaaacag 221
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100.0%; Pred. No. 5.3e-118;
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773 c 876 g 773
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Sequence 1 from Patent WO0183746.
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  876 9
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AX351029.1 GI:18616385
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ORIGIN
  ٥
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  'n
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   AUTHORS
TITLE
  DEFINITION
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   ACCESSION
VERSION
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  REFERENCE
   ACCESSION
   VERSION
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  REFERENCE
  AUTHORS
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   FEATURES
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 ${\tt IMPORTANT}$ : This sequence is not the entire insert of clone RP11-217B7 It may be shorter because we sequence overlapping

of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6

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ö
  121 getttgeteettgtttttteeeeggttetgtttteteeetteteeggaaggettgteaa 180
  0; Gaps
   1 gtaattgcgagcgagagtgagtggggccgggagccgcagagccgagccgaccttctctc 60
   8 GTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCTTCTCTC
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  Indels
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Live 0; Mismatches 0;
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1765 c 1905 g 1756 t
 Patent: WO 0170810-A 3 27-SEP-2001;
Bayer Aktiengesellschaft (DE)
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                               Location/Qualifiers
   Matches 221; Conservative
  Best Local Similarity
   1834 a
  Query Match
   BASE COUNT
ORIGIN
JOURNAL
                             FEATURES
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Human DNA sequence from clone RP11-217B7 on chromosome 9, complete Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 96717 bp AL359182.20 GI:18151453 (bases 1 to 96717) Homo sapiens sequence. AL359182 human. DEFINITION AL359182/C ORGANISM TITLE JOURNAL ACCESSION REFERENCE VERSION KEYWORDS AUTHORS SOURCE

linear PRI 11-JAN-2002

COMMENT

AL Shores I to 96/1/)

Skuce, C.

B ji (bases I to 96/1/)

Skuce, C.

B Direct Submission

Submitted (11-74N-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

on Jan 15, 2002 this sequence version replaced gi:18121468.

During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1-e., phred quality >-30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORNEPP; Information on the WORNEPP. http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RP11-217B7 is from the library RPCI-11.1 constructed by the group

```
sections only once, except for a short overlap.

The true right end of clone RPI1-217B7 is at 96717 in this sequence. The true left end of clone RPI1-122F10 is at 72980 in this sequence. The true right end of clone RPI1-132F10 is at 2000 in this sequence.
  ó
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 149034)
Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L., Cheng,J.F., Osorlio,J., Remaley,A., Yang,X.P., Haudenschild,C., Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N., Rublin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
  PRI 17-JUL-2000
  derived from a single pUC clone. Restriction digest data confirm the assembly." 92411...92557
   /note="Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data
   (AC026643). Assembly confirmed by restriction digest."
   92050. 92163 /note="Sequence from reads from a short insert library
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  /note="Sequence from AF275948 sequenced by National
Institutes of Heath, National Heart, Lung and Blood
Institute, Bethesda, MD 20892, USA."
  84249 .84273
/note="Sequence from overlapping clone RP11-122F10
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Homo sapiens ABCAl (ABCAl) gene, complete cds.
AF275948
   Db 17077 GGGGTAGGAGAAGGACGCAAACACAAAAGTGGAAAACAG 17037
  181 ggggtaggagaaagagacgcaaacacaaaagtggaaaacag 221
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100.0%; Pred. No. 5.5e-118;
iive 0; Mismatches 0;
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  ACCESSION
   REFERENCE
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AF275948
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   VERSION
  ORIGIN
   LOCUS
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Complete genomic sequence of the human ABCA1 gene; analysis of the human and mouse \mathtt{ATP}\textsc{-binding} cassette A promoter
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Santamarina-Fojo.s., Peterson,K.M., Knapper,C.L., Freeman,L.A.,
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Francois,T.L. and Brewer,H.B. Jr.
   Direct Submission
Submitted (08-JUN-2000) Molecular Disease Branch, National
Institutes of Heath, National Heart, Lung and Blood Institute,
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Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
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  Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 22, 2000 this sequence version replaced 91:6434033. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
  Center: Whitehead Institute/ MIT Center for Genome Research
  NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
  Mammalia; Euthería; Primates; Catarrhini; Hominidae; Homo.
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Assembly program: Phrap; version 0.960731

Consensus quality: 145749 bases at least Q40

Consensus quality: 145749 bases at least Q20

Consensus quality: 160940 bases at least Q20

Insert size: 185000; agarose-fp

Insert size: 171264; sum-of-contigs

Quality coverage: 2.9 in Q20 bases; sum-of-contigs
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Contact: sequence_submissions@genome.wi.mit.edu
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Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
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Qiu,Y., Caveller,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F. Human and mouse aboal comparative sequencing and transgenesis studies revealing novel regulatory sequences
Genomics 73 (1), 66-76 (2001)
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NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-8 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
                PRI 29-SEP-2000
   Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Tinjii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A. NEDO human CDNA sequencing project (Masuho, Y. and Oshima, A. Dipublished (2000)

2 (bases 1 to 1750)
Isogai, T. and Otsuki, T. Direct Submission (Masuho, Y. and Otsuki, T. Direct Submission (Masuho, Y. A., Masuho, Y. A., 
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   Query Match 99.1%; Score 219; DB 9; Length 1750; Best Local Similarity 100.0%; Pred. No. 7.8e-117; Matches 219; Conservative 0; Mismatches 0; Indels
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JOURNAL
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JOURNAL
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LOCUS
   REFERENCE
   AUTHORS
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AK022254
  RESULT
   VERSION
  COMMENT
   SOURCE
  q
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  ö
   133991 CCGGGCTGCGGCAGGCAGGCGGGGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGC 34050
  getitgeteettgittitteeeeggiteetgittieteeeetteteeggaaggetigieaa 180
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   34111
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   exon
   exon
  exon
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Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mall:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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  KEKLAAAERVLRSNMDILKPILMDVACDDIAHGQLTVPRSAAVATGGAKPNMAGRET
LLSICASVPKVEFHERHILEHFSFCVCVSVSLFPAKGIVSFSWASFRIWVLWKAVFWQ
HGESMAVWEGQLGLGLNIAFEYFTSIDVG"
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   Isogal,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Araase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,Y., Togiya,S., Kawai,F., Saito,K., Takeuchi,K., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A. Unpublished (2000)

2 (bases 1 to 1556)
Isogai,T. and Otsuki,T.
  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  125 tgctccttgtttttccccggttctgttttctccccttctccggaaggcttgtcaagggg 184
   Gaps
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Best Local Similarity
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  BASE COUNT
ORIGIN
   REFERENCE
AUTHORS
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   JOURNAL
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RESULT 13

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PAT 15-MAY-2001
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  PAT 30-MAY-2001
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Denefie, P., Rosier-Montus; M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H., Remalcy, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and diagnostic application
Patent: WO 0130848-A 70 03-MAY-2001;
  Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bassa 1 to 9854)
Denefie, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Maudin, L., Lemoine, C., Duverger, N., Jaye, M., searfoss Iii, G.H., Remaley, A., Brewer, H.B. and Dean, M.
Nucleics acids of the human abc1 gene and their therapeutic and diagnostic application
Patent: Ep 1096012.A 70 02-MAY-2001;
Aventis Pharma S.A. (FR)
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100.0%; Pred. No. 1.2e-108;
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   FEATURES
   KEYWORDS
  TITLE
  FEATURES
  VERSION
  TITLE
  SOURCE
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HTG 13-JUL-2000
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  Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 Lhis sequence version replaced gi:6705871.
All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasKer.html
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 69570)
  ....- Genome Center Center Center for Genome Research
  77 cagggcggggagctccgcgcaccaacagagccggttctcagggcgctttgctccttgttt 136
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                                 ó
Length 9854;
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  Contact: sequence_submissions@genome.wi.mit.edu
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 92.8%; Score 205; DB 6; L6 100.0%; Pred. No. 1.2e-108; ive 0; Mismatches 0;
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   AUTHORS
   AUTHORS
   COMMENT
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  g
  δλ
   g
   δ
  qq
   δy
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arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
  However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
contigs. Runs of N are used to separate the reads and the order in which they appear is completely
  11323 11422: gap of 100 bp 11423 12302: contig of 880 bp in length 12403 12402: gap of 100 bp 12403 13281 13281 13281 13281 1441: contig of 878 bp in length 13281 13380: gap of 100 bp 14342 14341: gap of 100 bp 14342 14341: gap of 100 bp 14342 14341: gap of 100 bp 14342 1436: contig of 855 bp in length
  29592: gap of 100 bp 30455: contig of 863 bp in length 30555: gap of 100 bp
   p of 100 bp contig of 848 bp in length tp of 100 bp contig of 853 bp in length
   70: gap of 100 bp
26621: contig of 851 bp in length
21: gap of 100 bp
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9530: gap of 100 bp
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872 971: gap of 100 bp

972 1834: contig of 863 bp in length

1835 1934: gap of 100 bp

1935 2804: contig of 870 bp in length

2805 2904: gap of 100 bp

2805 2904: gap of 100 bp

2805 2904: gap of 100 bp
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  of 100 bp contig of 800 bp in length
   of 100 bp contig of 870 bp in length
   p of 100 bp
contig of 868 bp in length
  bp
7 bp in length
  of 100 bp contig of 855 bp in length
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   65: gap of 100 bp 22832: contig of 867 bp in length
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contig of 827 bp
   contig of 837 bp
  100 bp
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19966: contig of 857
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17072: con+4
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30456 30555; gap of
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   24833: gap of
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   gap of
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  17172: gap of
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8580 9430; cor
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3846 4696: cor
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7510 7609: gap of
7610 8479: cor
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1 6540:
  [ 6640; gap c
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  58230: gap of 100 bp 59082: contig of 852 bp in length 59182: gap of 100 bp 60020: contig of 838 bp in length
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contig of 863 bp in length

ap of 100 bp

contig of 852 bp in length
  in length
  62035; gap of 100 bp
62866: contig of 831 bp in length
62966; gap of 100 bp
   64783: contig of 856 bp in length
  p of 100 bp contig of 867 bp in length
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   64883: gap of 100 bp
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31410: contig of 855 bp
31510: gap of 100 bp
32368: contig of 858 bp
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61935: ~
.35
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60983: cont
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56298 571
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I (bases I to 18399)

Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M. Compositions and methods for modulating hdl cholesterol and triglyceriae levels
Patent: WO 0115676-A I 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)

Location/Qualifiers
  41565 GTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTC 41624
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   ó
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100.0%; Pred. wc.
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Matches 201; Conservative
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  REFERENCE
AUTHORS
TITLE
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   PAT 22-JAN-2001
             PAT 22-JAN-2001
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10442)

Lawn,R.M., Wade,D. and Garvin,M.

Regulation with binding cassette transporter protein abcl

Patent: WO 0078972-A 1 28-DEC-2000;

CV THERAPEUTICS, INC. (US)
   Eukaryogia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Lawn.R.M., Wade,D., Oram.J.F. and Garvin,M.

Atp binding cassette transporter protein abcl polypeptides Patent: WO 0070871-A 1 28-DEC-2000; CV THERAPEUTICS, INC. (US)
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AX060892
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  δX
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  ВÞ
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  Therefore, Ton 10442)

Lawn, R.M., Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,

Lawn, R.M., Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,

Direct Submission

Submitted (Ge-JUL-2000) Discovery Research, CV Therapeutics Inc.,

3172 Porter Drive, Palo Alto, CA 94304, USA
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Gaps

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89.1%; Score 197; DB 6; Length 10442; 100.0%; Pred. No. 5.9e-104; Live 0; Mismatches 0; Indels 0

Best Local Similarity 100. Matches 197; Conservative

Query Match

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COMMENT

2898 a BASE COUNT ORIGIN

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Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING. AC021345.2 GI:9130845 HTG; HTGS DUNACE human. AC021345/c DEFINITION ORGANISM ACCESSION KEYWORDS SOURCE VERSION RESULT LOCUS

HTG 13-JUL-2000

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliais Euthenia; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 90698) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-24J9 Unpublished (bases 1 to 90698) JOURNAL REFERENCE REFERENCE AUTHORS AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Gartelugh, W., Forresto, G., Gaqe, D., Galagan, J., Gartelugh, W., Forresto, G., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Hadsord, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,

Macdonald, P., Marguis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollar's, V. Raymond, C., Riley, R., Rothman, D., Stojanovic, N., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct Submission Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced 91:6705761.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html ..... Genome Center Center: Whitehead Institute/ MIT Center for Genome Research NOTE: This record contains 92 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence\_submissions@genome.wi.mit.edu the record is updated, the accession number will 911 1010: gap of 100 bp 1011 1873: contig of 863 bp in length 1874 1973: gap of 100 bp 910: contig of 910 bp in length Project Information Center project name: L4483 Center clone name: 24\_J\_9 be preserved. TITLE JOURNAL

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Regulation with binding cassette transporter protein abcl
Regulation with binding cassette transporter protein abcl
Patent: Wo 0078972-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)

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BASE COUNT

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abc1 polypeptides
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CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
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Regulation with binding cassette transporter protein abcl
Patent: W0 0078972. A 9 28 DEC-2000;
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DEFINITION

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1 (bases 1 to 446)
Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Jaye,M., searfoss Iil,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
Nucleics acids of the human abcl gene and their therapeutic and
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1 (bases 1 to 446)
Denefile, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H., Remaley, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and diagnostic application
Nucleic acids of the human abcl gene and their therapeutic and parent: WO 0130848+3 303-MAY-2001;
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Patent: BP 1096012-A 3 02-MAY-2001;
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I (bases 1 to 9741)

Denefle, P., Rosier-Montus, M. F., Arnould-Requigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H., Nucleic acids of the human abcl gene and their therapeutic and adaquostic application
Patent: WO 0130848-A 69 03-MAY-2001;
Aventis Pharma S.A. (FR)

Location/Qualifiers
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  JOURNAL
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   Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S. Regulatory nucleic acid sequences of the abcl gene Patent: WO 0183746-A 10 08-NOV-2001;
Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., searfoss Iii, G.H., Remaley, A., Brewer, H.B. and Dean, M.
Nucleics acids of the human abcl gene and their therapeutic and diagnostic application
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PAT 22-JAN-2001
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Lawn, R.M., Wade, D. and Garvin, M.
Esquiation with binding cassette transporter protein abcl Patent: WO 0078972-A 3 28-DEC-2000; CV THERAPEUTICS, INC. (US)
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**Lap binding cassette transporter protein abc1 polypeptides
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in length

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18 38183: gap of 100 bp
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  Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Bouguslawity, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gadae, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Hedrod, A., Horton, L., Landers, P., Fitzhugh, W., Forrest, C., Gage, D., Cooke, F., Landers, T., Lehorczky, J., Levine, R., Lieut, G., Looke, K., Macdonald, P., Marquis, N., Meneus, L., Morrow, J., Naylor, J., Morheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donneill, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rohman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Hyman, D., Ye, W.J., Lester, M., A., And Zody, M., Lanmas, J., Tesfaye, S., Theodore, J., Zimmer, A. and Zody, M.
  Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced g1:6705871. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I bases 1 to 69570)

Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome, clone RP11-1N10
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Center: Whitehead Institute/ MIT Center for Genome Research
   sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
   Contact: sequence_submissions@genome.wi.mit.edu
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JOURNAL
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AUTHORS
  JOURNAL
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COMMENT

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Submitted (18-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, 06 3108, USA (Bases 1 to 92227) Waterston,R.H.
  Direct Submission
Submitted (29-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
   Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
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ACU22563
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Contact: submissions@watson.wustl.edu
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   Direct Submission
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   9 €
   source
  REFERENCE
AUTHORS
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us-09-846-456-4.oli.rge

TITLE JOURNAL COMMENT

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Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGluk, J., McPheeters, R., Marquis, N., McEwan, P., McGluk, J., Maylor, J., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pisan, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Santos, R., Severy, P., Spencer, B., Stange-Thomann, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vasiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Alley, R., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Mitchead Institute/MIT Center for Genome Submitted (06-FBE-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6910806.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1995-1997)
   Center: Whitehead Institute/ MIT Center for Genome Research
   sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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  5416:
   6968;
  7757:
   2305:
  3113:
   9336:
   4646:
  6193:
   3867
  8657:
  2405:
  3213:
   3967:
  4746:
  5516:
   7068:
  7857:
   9436:
   6293:
  be preserved.
  10125
   11664 :
11764
  3114
   1493
   3868
  5417
5517
6194
6294
6969
  7758
  0880
  2306
  8558
8658
9337
9437
   4647
  0860
  690
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22671: contig or vo. v. 2771: gap of 100 bp 23451: contig of 680 bp in length 23451: contig of 680 bp in length 100 bp 24267: contig of 706 bp in length 24367: gap of 100 bp 25073: contig of 706 bp in length 4 25173: gap of 100 bp 100 bp 25667: contig of 708 bp in length 18 25667: contig of 694 bp in length 18 25667: contig of 702 bp in length 10 2669: contig of 676 bp in length 10 2769: gap of 100 bp 10 100 tp 10 2769: gap of 100 bp 10 2769: gap of 100 bp 10 2769: gap of 100 bp 10 2769: gap of 100 bp 10 2769: gap of 100 bp 10 2769: gap of 100 bp 10 2769: gap of 100 bp 10 2769: gap of 100 bp 10 2769: gap of 100 bp 10 2769: gap of 100 2769: ga
   41659: contig of 689 bp in length
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42434: contig of 675 bp in length
42534: gap of 100 bp
43207: contig of 673 bp in length
   in length
   in length
  in length
   in length
   01: gap of 100 bp 18493: contig of 692 bp in length 193: gap of 100 bp 18274: contig of 681 bp in length
  in length
                         in length
   in length
  in length
  in length
   in length
   in length
  in length
  in length
   in length
   in length
   in length
  in length
  in length
  in length
9 14898: gap of 100 bp
15571: contig of 673 bp in
2 15671: gap of 100 bp
1 1587: contig of 100 bp
8 16487: gap of 100 bp
8 17198: contig of 711 bp in
   20320: contig of 665 bp 11

20120: gap of 100 bp

21112: contig of 692 bp 11

212: gap of 100 bp

21865: contig of 673 bp 11

985: gap of 100 bp

22671: contig of 686 bp 11
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327; gap of 100 bp
32168; contig of 711 bp 11
268; gap of 100 bp 1
32951; contig of 683 bp 11
051; gap of 100 bp 11
33756; contig of 705 bp 11
  : contig of 679 bp 10

iap of 100 bp in a point of 678 bp in a point of 678 bp in a point of 683 bp in a point of 683 bp in a contig of 686 bp 11.
  ابط ر
موم ر
   100 bp
  100 bp
686 bp
  43: gap of 100 bp
36924: contig of 681 bp
24: gap of 100 bp
37701: contig of 677 bp
  40171: gap of 100 bp
40870: contig of 699 bp
40970: gap of 100 bp
  156: gap of 100 bp 34566: contig of 710 bp 166: gap of 100 bp 35376: contig of 710 bp
  contig of 710 bp
p of 100 bp
contig of 667 bp
   p of 100 bp contig of 697 bp
  o of 100 bp contig of 710 bp
  contig of 664 bp
o of 100 bp
contig of 683 bp
   30571: contig of 686
  100
   15572 15671: gap of
15672 16387: cont
  30671: gap of
  33051: gap of
33756: cont
   39374: gap of
40071: cont
  17298: gap of
18008: con
   18108: gap of
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   19655: gap of
   29102: gap of
   21985: gap of
   28324: gap of 29002: con
   gap of
   gap of
   gap of
  19555:
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  20420:
   36243:
  37801:
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  21212:
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  37024:
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  31458 32169
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Shren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Bairen, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Donino, M., Poyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Haefford, A., Horton, L., Howland, J.C., Lilev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., Meheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   Gaps
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   27: gap of 100 bp
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   p of 100 bp contig of 691 bp in length p of 100 bp contig of 570 bp in length
  21: gap of 100 bp
55702: contig of 681 bp in length
02: gap of 100 bp
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   Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 10, clone RP11-524H12
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   50432: gap of 51127: cont
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  44868: gap of
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AUTHORS
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   AUTHORS
  JOURNAL
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   TITLE
   VERSION
   SOURCE
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   Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced gi:7637299.
   Center: Whitehead Institute/ MIT Center for Genome Research
  NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Consensus quality: 154128 bases at least Q40
Consensus quality: 158489 bases at least Q30
Consensus quality: 160079 bases at least Q20
Insert size: 160000; agarose-fp
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Quality coverage: 4.7 in Q20 bases; sum-of-contigs
  All repeats were identified using RepeatWasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatWasker.html
   Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads
  Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: project Information
Center project name: 18340
Center clone name: 524_H_12
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   p of 100 bp contig of 12461 bp in length
   70581; gap of 100 bp 80819; contig of 10238 bp in length 80919; gap of 100 bp 91740; contig of 10821 bp in length
  113944 114043: gap of 100 bp
114044 137119: contig of 23076 bp in length
137120 137219: gap of 100 bp
  p of 100 bp
contig of 22103 bp in length
   882 981: gap of 100 bp

982 4366: contig of 3385 bp in length

4367 4466: gap of 100 bp

7421 7520: contig of 2954 bp in length

7421 7520: gap of 100 bp

7521 11683: contig of 4163 bp in length
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   o of 100 bp contig of 8516 bp in length
  11783: gap of 100 bp 15264: contig of 3481 bp in length
   15364: gap of 100 bp 20920: contig of 5556 bp in length
   881: contig of 881 bp in length
  36585; c
   58020: gap of
70481: cont
   21020: gap of
27969: cont
  91840: gap of
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   28069:
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JOURNAL
   COMMENT
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   Submitted (23-0CT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Aug 31, 2000 this sequence version replaced gi:7690207.
Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
  Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
  Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
  This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
   Gaps
  * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced
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gap of unknown length
contig of 13982 bp in length.
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100.0%; Pred. No. 2.4;
ive 0; Mismatches (
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Matches 20; Conservative
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187857
187957
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AUTHORS
TITLE
  BASE COUNT
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  JOURNAL
 JOURNAL
   FEATURES
   COMMENT
   LOCUS
  δλ
   ó
  AC012325 201938 bp DNA linear HTG 25-APR-2001
Homo sapiens chromosome 16 clone RP11-93H5, WORKING DRAFT SEQUENCE,
   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
   Gaps
   ;
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. The exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Dembic, Z., Garotta, G. and Gentz, R.H.
Chimeric human interferon-gamma-receptor/immunoglobulin
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Pred. No. 2.4;
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Other publication JP 6319552 941122
Other publication NZ 250997 951026
Other publication CA 2114168 940906
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   Submitted (13-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Dec 20, 2001 this sequence version replaced g1:17062530.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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  Assembly program: Phrap; version 0.990329First call to
   Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
   Center: Baylor College of Medicine
  Center project name: GIOR
Center clone name: CH230-152G15
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HTG; HTGS_PHASE1; HTGS_DRAFT.
   Unpublished
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Gaps

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HUMIFNRG/C
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VERSION
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AUTHORS
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MEDLINE
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   VERSION
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   ACCESSION
  REFERENCE
   AUTHORS
  MEDLINE
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Homo sapiens clone YAN1 interferon-gamma receptor mRNA, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1641)
Allende, L.M., Lopez-Goyanes, A., Paz-Artal, E., Corell, A.,
Gancia-Perez, M.A., Varela, P., Scarpellini, A., Negreira, S.,
Palenque, E. and Arnaiz-Villena, A.
A point mutation in a domain of gamma interferon receptor 1
provokes severe immunodeficiency
Clin. Diagn. Lab. Immunol. 8 (1), 133-137 (2001)
   2 (bases 1 to 1641)
Arnalz-Villena,A.
Direct Submission
Submitsion (02-APR-1998) Immunology, Hospital 12 de Octubre, Crta.
Andalucia Km. 5.4, Madrid 28041, Spain
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2064)
Aguet, M., Dembic, Z. and Merlin, G.
   Simian immunodeficiency virus (clone agm49gag) gag gene, complete
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(bases 1 to 1773)

(this ch, V.M., McGann, C., Dapolito, G., Goldstein, S., Ogen-Odoi, A., Biryawaho, B., Lakwo, T. and Johnson, P.R.
Identification of a new subgroup of SIVagm in tantalus monkeys Virology 197, 426-430 (1993)
  Molecular cloning and expression of the human interferon-gamma
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  Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
   ö
   ô
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Fountoulakis,M., Garotta,G. and Stueber,D. Solubbe interferon-gamma receptors and methods for their production Patent: EP 0393502-A 1 24-0CT-1990; F. HOFFMANN-LA ROCHE AG
   PAT 06-AUG-1996
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  SOURCE
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
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Web site: http://www-shqc.stanford.edu
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   ö
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2127)
  Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
  Submitted (27-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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